

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 24, 2003, 11:50:09 ; Search time 38 Seconds  
(without alignments)  
981.847 Million cell updates/sec

Title: US-09-993-420A-3

Perfect score: 1479  
Sequence: 1 MTRCTADNSLTNPATRRRTM.....ACATGIVGVVCGRMFLSK 280

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

A\_Geneseq\_101002:\*

- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*
- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*
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- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*
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- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*
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- 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*
- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1476	99.8	280	15	AAAR7343
2	161.5	10.9	192	20	AAAY05533
3	151	10.2	192	20	AAW97393
4	151	10.2	193	19	AAW61391
5	151	10.2	193	20	AAAY05531
6	151	10.2	193	20	AAW97391
7	150	10.1	193	20	AAAY05530
8	148	10.0	192	20	AAW97394
9	148	10.0	193	18	AAW6047
10	148	10.0	193	19	AAW61392

11	148	10.0	193	20	AAAY05532
12	148	10.0	193	20	AAW97392
13	145.5	9.8	168	18	AAW36048
14	138	9.3	233	22	AAW73304
15	136	9.2	411	22	AAU00219
16	135.5	9.2	225	18	AAW19396
17	135	9.1	233	16	AAW68887
18	135	9.1	233	17	AAW05821
19	135	9.1	233	18	AAW31530
20	135	9.1	233	21	AAW83223
21	135	9.1	233	21	AAW69969
22	135	9.1	233	22	AAW64262
23	135	9.1	233	22	AAW73303
24	135	9.1	233	22	AAW50538
25	135	9.1	233	22	AAW47515
26	126.5	8.6	212	22	AAW64285
27	126	8.5	365	19	AAW58884
28	120.5	8.1	232	17	AAW01019
29	120.5	8.1	232	20	AAW94346
30	119.5	8.1	232	17	AAW01020
31	119.5	8.1	232	20	AAW94347
32	118.5	8.0	236	22	AAW35131
33	118.5	8.0	236	22	AAW76554
34	117.5	7.9	485	22	AAU00222
35	117	7.9	239	20	AAW01018
36	117	7.9	239	20	AAW94345
37	116	7.8	239	20	AAW87810
38	116	7.8	239	22	AAW74127
39	116	7.8	239	22	AAW48288
40	116	7.8	239	22	AAW35130
41	116	7.8	239	22	AAW50537
42	116	7.8	239	23	AAU076553
43	115	7.8	239	15	AAW47344
44	115	7.8	239	17	AAW02383
45	114.5	7.7	212	22	AAW20495

#### ALIGNMENTS

RESULT 1  
AAAR7343  
ID AAAR7343 standard; Protein; 280 AA.  
XX  
AC AAAR7343;  
XX  
XX  
DT 23-JUN-1994 (first entry)  
XX  
DE ced-9 protein.  
XX  
XX Cell death; senescence; programmed cell death; ced-9; myocardial  
XX infarction; stroke; brain injury; neurodegenerative disease;  
XX muscular degenerative disease; ageing; hypoxia; ischaemia; toxemia;  
XX infection; hair loss; neoplasia; cancer; ced-3; ced-4; bcl-2;  
XX oncogene.  
XX  
XX Caenorhabditis elegans.  
XX  
XX W09325683-A.  
XX  
XX  
XX 23-DEC-1993.  
XX  
XX  
XX 14-JUN-1993; 93WO-US05651.  
XX  
XX 12-JUN-1992; 92US-0898933.  
XX 10-AUG-1992; 92US-0927681.  
XX  
XX (MAST) MASSACHUSETTS INST TECHNOLOGY.  
XX Hengartner M, Horvitz HR;  
XX WPI, 1994-007540/01.  
XX N-PSDB; AA054630.  
XX DR

Human Bcl-w protei  
The human bcl-y pr  
Mouse bcl-w protei  
Mutant rat Bcl-XL  
Bcl-XL-DPR apoptos  
"Deprenyl" (RTM)-1  
Human thymus Bcl-X  
Bcl-XL protein. H  
Human anti-apoptot  
Bcl-x polypeptide.  
Human Bcl-XL prote  
Human Bcl-XL prote  
Rat wild-type Bcl-  
Human Bcl-XL prote  
Protein encoded by  
Mutant bcl-XL prot  
Amino acid sequenc  
Apoptosis-blocking  
Human Bcl-2 mutant  
Apoptosis-blocking  
Human Bcl-2 mutant  
Murine Bcl-2. Mus  
Murine Bcl-2 polyp  
Ltn-Bcl-XL apoptos  
Apoptosis-blocking  
Human Bcl-2 wild-t  
A human Bcl-2 prot  
Human Bcl-2. Homo  
Human Bcl-2. Homo  
Human Bcl-2. Homo  
Human Bcl-2. Homo  
Human Bcl-2. Homo  
Human Bcl-2. Homo  
Human Bcl-2 polype  
Human oncogene bcl  
Human BCL2. Homo  
Human Bcl-XL (tran

XX Caenorhabditis elegans cell death-protective gene - used to  
 PT develop agents for preventing cell death or for reducing  
 PT population of cells  
 XX  
 PS Claim 5; Page 59-60; 112pp; English.  
 XX  
 CC ced-9 is essential for C. elegans development and apparently  
 CC functions by protecting cells during development from programmed  
 CC cell death. ced-9 was shown to function by antagonising the  
 CC activities of cell death genes ced-3 and ced-4. The protein product  
 CC of the human oncogene bcl-2 was found to have a similar sequence  
 CC to the ced-9 protein. The ced-9 gene can be used for developing  
 CC agents for treating a condition characterised by increased cell death  
 CC such as myocardial infarction, stroke, traumatic brain injury,  
 CC neurodegenerative disease, muscular degenerative disease, ageing,  
 CC hypoxia, ischaemia, toxemia, infection or hair loss. It can also  
 CC be used for reducing a population of cells in the treatment of  
 CC neoplastic growth cancerous tissue, infected cells or autoreactive  
 CC immune cells.  
 CC  
 SQ Sequence 280 AA;  
 XX  
 Query Match 99.8%; Score 1476; DB 15; Length 280;  
 Best Local Similarity 99.6%; Pred. No. 5.3e-160;  
 Matches 279; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKGTPEPTDEGINSADADLPSPSRQASTRRM 60  
 DB 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKGTPEPTDEGINSADADLPSPSRQASTRRM 60  
 QY 61 SIGESIDGKINDMEEPRLDIEGFVDFYTHIRIRONGMEMFGAPGLPCGVOPPEHEMRVWG 120  
 DB 61 SIGESIDGKINDMEEPRLDIEGFVDFYTHIRIRONGMEMFGAPGLPCGVOPPEHEMRVWG 120  
 QY 121 TIFEKKAENPFEPCBELLAVPRISFSLYODVVRTVGNADTDCPMSTYGRLLISFGGR 180  
 DB 121 TIFEKKAENPFEPCBELLAVPRISFSLYODVVRTVGNADTDCPMSTYGRLLISFGGR 180  
 QY 181 VAAKMMSEVELQGVNRLFVYTSLFKTRIRNNMKEHNSWDDFMTLGKMKEDYERAE 240  
 DB 181 VAAKMMSEVELQGVNRLFVYTSLFKTRIRNNMKEHNSWDDFMTLGKMKEDYERAE 240  
 QY 241 EKYGRKRONRMSMIGAGVAGAIYGVVCGRRMFSK 280  
 DB 241 EKYGRKRONRMSMIGAGVAGAIYGVVCGRRMFSK 280

RESULT 2  
 ID AAY05533 standard; Protein; 192 AA.  
 XX  
 AC AAY05533;  
 XX  
 DT 05-JUL-1999 (first entry)  
 XX  
 DE Mouse Bcl-w protein derivative.  
 XX  
 KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;  
 KW animal model.  
 XX  
 OS Mus sp.  
 XX  
 PN W09913710-A1.  
 XX  
 PD 25-MAR-1999.  
 XX  
 PF 16-SEP-1998; 98WO-AU00764.  
 XX  
 PR 16-SEP-1997; 97AU-0009228.  
 XX  
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
 XX

PI Adams J, Cory S, Gibson L, Koentgen F, Print C;  
 XX  
 DR WPI; 1999-243890/20.  
 DR N-PSDB; AAX25135.  
 XX  
 PT An animal model exhibiting reduced levels of a Bcl-w protein and/or  
 PT protein associated with Bcl-w  
 XX  
 PS Disclosure; Page 39; 52pp; English.  
 XX  
 CC The present sequence is described of a derivative of mouse Bcl-w  
 CC (see also AAY0531), a pro-survival member of the Bcl-2 family that  
 CC is widely expressed and which is essential for spermatogenesis.  
 CC The derivative lacks the 24 N-terminal amino acids of Bcl-w.  
 CC The invention relates generally to a method of treatment and to an  
 CC animal model for the identification of molecules and genetic  
 CC sequences useful for inducing or reducing fertility of male animals.  
 CC Methods are provided for the treatment of infertility, or for  
 CC reducing fertility, by modulating spermatogenesis. An animal model  
 CC carries a mutation is at least one allele of the human or murine  
 CC bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w.  
 CC Such animals have disorganised seminiferous tubules and are  
 CC substantially infertile, but possess no other major abnormalities  
 CC as determined by histological examination. They can be used to  
 CC screen for therapeutic molecules including genetic sequences  
 CC capable of inducing, enhancing or otherwise facilitating  
 CC spermatogenesis in animals, or which can induce infertility.  
 CC  
 SQ Sequence 192 AA;  
 XX  
 Query Match 10.9%; Score 161.5; DB 20; Length 192;  
 Best Local Similarity 25.6%; Pred. No. 8.1e-10;  
 Matches 54; Conservative 29; Mismatches 89; Indels 39; Gaps 8;  
 QY 79 DIEGFVDFYTHIRIRONGMEMFGAPGLPCGVOPPEHEMRVWGTFEKKHAENPFEPCBOL 138  
 DB 9 DTRALVADPVGTRLNOKGYVCAGGEGPADPLQANRAAGDEFETFRRTFSDLAQL 68  
 QY 139 IAVP-----RISFSLYODVVRTVGNADTDCPMSTYGRLLISFGFVAARM--ES 188  
 DB 69 HTVPSAQQRFQVSDLEFG-----GPNNGRIAVFVFGAALCAESVNM 115  
 QY 189 VELQGVNRLFVYTSLFKTRIRNNMKEHNSWDDFMTL-GKMKEDYERAEKVRK 247  
 DB 116 EPLVQVQDWTY--AYLETRLA-DWHSQGMADFTALYDGALED-----ARRL 162  
 QY 248 ONRMSMIGAGVAGAIYGVVCGRRMFS 278  
 DB 163 REGNMAY--STVYTGAVAGALVYGAFFAS 191

RESULT 3  
 ID AAM97393 standard; Protein; 192 AA.  
 XX  
 AC AAM97393;  
 XX  
 DT 20-MAY-1999 (first entry)  
 XX  
 DE Protein sequence of the specification.  
 XX  
 KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
 KW premature cell death; cell death stimulator; prolonged cell life span;  
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;  
 KW parasite.  
 KW  
 OS Unidentified.  
 XX  
 PN US5883229-A.

Query Match	Best Local Similarity	Score	DB	Length
Matches 51; Conservative 31; Mismatches 92; Indels 36; Gaps 8	10.2%;	151;	DB 20;	Length 192;
	24.3%;	Pred. No. 1.3e-08;		
79 DIEGEVVDYFTIRIRONGEMFEGAPGLPCGVDPHEHMKVMGTFIEFKKAENFETCEOL 138	11	11	11	11
8 DFRALVADDEVGYKLRQKGGVCCAGPEGCPAADPLHQMAMRAAGDEFTRRRTFSDLAOL 67	11	11	11	11
139 LAMP-----RISLSLODVYRTVGNMOTDCCPSYGLILISFGGFVAAKM--ES 188	11	11	11	11
68 HTVPGSAQORFVOVSELDG-----GNNMGRILVAFYFPGALCAESYNNKM 114	11	11	11	11
189 VELQGVNRNLEVYTSLEFIRIRNNKKEHNRNSWDEPMLTGKQNKEDYERAEAEKVGRKKO 248	11	11	11	11
115 EPLVGVQVDMV--TYLETRILA-DWTHSGGWAFFTAL-----YGDGLTEE-ARRUR 162	11	11	11	11
249 NRRWSMIGAGYTAGAIGCVVYCGMMPS 278	11	11	11	11
163 EGNMASVTR-VLTGVAVALGALTGTGAFPAS 191	11	11	11	11

RESULT 4  
AA61391  
ID AA61391 standard; Protein; 193 AA.

AA61391;  
AC  
DT 02-OCT-1998 (first entry)  
XX  
DE Rat bcl-y protein.  
XX  
XX bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.

[illegible]

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XX PD 25-MAR-1999.
XX PF 16-SEP-1998: 98MO-AU00764.
XX PR 16-SEP-1997: 97AU-0009228.
XX PA (HAL-) HALI INST MEDICAL RES WALTER & ELIZA.
XX PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
XX DR WPI: 1999-243890/20.
XX DR N-PSDB; AAX25133.
XX PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
XX PT protein associated with Bcl-w
XX PS
XX PS Claim 2: Page 35; 52pp; English.
XX CC The present sequence is mouse Bcl-w, a pro-survival member of the
XX CC Bcl-2 family which is widely expressed and which is essential for
XX CC spermatogenesis. The invention relates generally to a method of
XX CC treatment and to an animal model for the identification of
XX CC molecules and genetic sequences useful for inducing or reducing
XX CC fertility of male animals. Methods are provided for the treatment
XX CC of infertility, or for reducing fertility, by modulating
XX CC spermatogenesis. An animal model carries a mutation is at least
XX CC one allele of the human or murine bcl-w gene (see AAX25132-35) or in
XX CC a gene associated with bcl-w. Such animals have disorganised
XX CC seminiferous tubules and are substantially infertile, but possess no
XX CC other major abnormalities as determined by histological examination.
XX CC They can be used to screen for therapeutic molecules including
XX CC genetic sequences capable of inducing, enhancing or otherwise
XX CC facilitating spermatogenesis in animals, or which can induce
XX CC infertility.
XX
XX Sequence 193 AA:
XX
Query Match 10.2%; Score 151; DB 20; Length 193;
Best Local Similarity 24.3%; Pred. No. 1.3e-08;
Matches 51; Conservative 31; Mismatches 92; Indels 36; Gaps
OY 79 DIEGFWVDIFTHIRONGEMWEGAGLPGCVGPEHEHMMVMTGTFEKKHAENFEFTCEBL 138
DB 9 DTRALVADPVGKIKLKQKGYCGAGCEGCPADPLHOAMRAADDEFTRRRFFSDIAQL 68
OY 139 LAVP-----RISFSLYQDVVTRTVGNAQTDCPMSYGLRLGLISFGGFVAKMM--ES 188
DB 69 HVTPESSAQQRFQVQSDLEFG-----SPNMGRLVAFVFGAALCAESYNKEM 115
OY 189 VELGQGVRLRYFTYSLFETKTRIRNMKKEHNSWMDPMTLGKMKEDYEAEAEKGRKKQ 248
DB 116 EPLVQGVQDMNV---AYLETRLA-DMIHSSGGWAETPAL-----YGDGALEE-ARRLR 163
OY 249 NNRWSMIGAGYTAGAIGIVGVVCGRMMS 278
DB 164 EGNMASVTR-VLTGAVALGALVTGCAFFAS 192
RESULT 6
AAM97391
ID AAM97391 standard; Protein, 193 AA.
XX AC AAM97391;
XX DE 20-MAY-1999 (first entry)
XX DE The rat bcl-y protein.
XX
XX Rat bcl-y protein; Bcl-y; human bcl-y protein; Bcl-y; bcl-2 homologue;
XX programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
XX head trauma; Alzheimer's disease; neural; muscular degenerative disease;
XX multiple sclerosis; myocardial infarction; vitally induced cell death.

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KM	aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KM	premature cell death; cell death stimulator; prolonged cell life span;
KM	Kaposi's sarcoma; lung cancer; autoimmune, hyperimmune disease;
KM	parasite.
XX	
OS	Rattus sp.
XX	
PN	US5883229-A.
XX	
PD	16-MAR-1999.
XX	
PF	25-NOV-1997; 9705-0978523.
XX	
PR	23-FEB-1996; 9605-0012201.
PR	11-FEB-1997; 9705-0798897.
PR	25-NOV-1997; 9705-0978523.
XX	
PA	(COCE-) COCENSYS INC.
XX	
PI	Guastella J;
XX	
DR	WPI; 1999-214150/18.
DR	N-PSDB; AAX15945.
XX	
PT	Novel bcl-y homologues of the rat and human bcl-2 protein - useful for modulating programmed cell death

CC The present sequence represents rat bcl-*y* protein (Rbcl-*y*). The  
CC specification also describes human bcl-*y* protein (Hbcl-*y* and  
CC Hbcl-*y* are homologues of the bcl-2 protein thought to be involved in  
CC programmed cell death (apoptosis and necrosis). Rbcl-*y* and Hbcl-*y*  
CC proteins may be used to treat conditions associated with a disruption of  
CC the cell death pathway. If they act as cell death inhibitors, they may be  
CC used in therapies to treat subjects suffering from: strokes, head trauma,  
CC Alzheimer's Disease, neural and muscular degenerative diseases  
CC (especially multiple sclerosis), myocardial infarction, vitally induced  
CC cell death, aging, spinal cord injuries and amyotrophic lateral  
CC sclerosis- conditions where cells under go premature cell death as a  
CC result of triggers which may or may not be apparent. They may also be  
CC used in this way to develop cell lines which remain viable in culture for  
CC an extended period. In contrast, if they act as cell death stimulators,  
CC Rbcl-*y* and Hbcl-*y* may be used to treat conditions associated with  
CC prolonged cell life span such as cancer (especially Kaposi's sarcoma and  
CC lung cancer) and auto/hyperimmune diseases. They may also be used to  
CC cause cell death in, and hence control, parasites.

[illegible]

ID AAV05530 standard; Protein; 193 AA.  
 AC AAV05530;  
 DT 05-JUL-1999 (first entry)  
 DE Human Bcl-w protein essential for spermatogenesis.  
 KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;  
 KW animal model.  
 OS Homo sapiens.  
 PN W09913710-A1.  
 PD 25-MAR-1999.  
 PE 16-SEP-1998; 98MO-AU00764.  
 PR 16-SEP-1997; 97AU-0009228.  
 PA (HALD-) HALL INST MEDICAL RES WALTER & ELIZA.  
 PI Adams J, Cory S, Gibson L, Koentgen F, Print C;  
 DR WPI: 1999-243890/20.  
 DR N-PSDB; AAX25132.  
 PT An animal model exhibiting reduced levels of a Bcl-w protein and/or  
 PS protein associated with Bcl-w  
 PS Claim 2; Page 33; 52pp; English.  
 CC The present sequence is human Bcl-w, a pro-survival member of the  
 CC Bcl-2 family which is widely expressed and which is essential for  
 CC spermatogenesis. The invention relates generally to a method of  
 CC treatment and to an animal model for the identification of  
 CC molecules and genetic sequences useful for inducing or reducing  
 CC fertility of male animals. Methods are provided for the treatment  
 CC of infertility, or for reducing fertility, by modulating  
 CC spermatogenesis. An animal model carries a mutation is at least  
 CC one allele of the human or murine bcl-w gene (see AAX25132-35) or in  
 CC a gene associated with bcl-w. Such animals have disorganised  
 CC seminiferous tubules and are substantially infertile, but possess no  
 CC other major abnormalities as determined by histological examination.  
 CC They can be used to screen for therapeutic molecules including  
 CC genetic sequences capable of inducing, enhancing or otherwise  
 CC facilitating spermatogenesis in animals, or which can induce  
 CC infertility.  
 CC XX  
 SQ Sequence 193 AA;  
 Query Match 10.1%; Score 150; DB 20; Length 193;  
 Best Local Similarity 24.3%; Pred. No. 1.7e-08;  
 Matches 51; Conservative 30; Mismatches 93; Indels 36; Gaps 8;  
 QY 79 DIEGFVVDYFTHIRONGEMWFGAGLPCGVPEHEMRVWGTTFEKKHAENFEFCOL 138  
 DB 9 DTRALVDEPVGKLRQKGYVCGAGPGCPADPLHQAMRAAGDEFEFRFRFTSDLAOL 68  
 QY 139 LAVP-----RISFSLYQDVVTVGNNAQTDCPSYGRLLIGLSFGFVAAKMM--ES 188  
 DB 69 HYPFGSAOQRFTQVDELFQG-----GPNCRILVAFVFGALCAESVNNEM 115  
 QY 189 VELQGVGNRLFYVYSLFTFTRIRNNKKEHNSWDDPMLGKOMKEDYERAEKVGRRKQ 248  
 DB 116 EPLVGVQVCEMNV--AYLETRLA-DWISSGGMAEFTEL-----YGDGALEE-ARRLR 163  
 QY 249 NRRWSMIGAGTAGAIGYGVVVGCMMS 278  
 DB 164 EGNMASVRT-VLTGAVALGALVTVGAFFAS 192

RESULT 8  
 ID AAW97394  
 ID AAW97394 standard; Protein; 192 AA.  
 AC AAW97394;  
 DT 20-MAY-1999 (first entry)  
 DE Mammalian bcl-y protein.  
 KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
 KW premature cell death; cell death stimulator; prolonged cell life span;  
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;  
 KW parasite.  
 OS Mammalia.  
 PN US5883229-A.  
 PD 16-MAR-1999.  
 PE 25-NOV-1997; 97US-0978523.  
 PR 23-FEB-1996; 96US-0012201.  
 PR 11-FEB-1997; 97US-0798897.  
 PR 25-NOV-1997; 97US-0978523.  
 PA (COCCE-) COCENSYS INC.  
 PI Guastella J;  
 DR WPI: 1999-214150/18.  
 PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful  
 PS for modulating programmed cell death  
 PS Claim 2; Columns 19-22; 26pp; English.  
 CC The present sequence represents a mammalian bcl-y protein.  
 CC The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y  
 CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein  
 CC thought to be involved in programmed cell death (apoptosis and necrosis).  
 CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated  
 CC with a disruption of the cell death pathway. If they act as cell death  
 CC inhibitors, they may be used in therapies to treat subjects suffering  
 CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular  
 CC degenerative diseases (especially multiple sclerosis), myocardial  
 CC infarction, vitally induced cell death, aging, spinal cord injuries and  
 CC amyotrophic lateral sclerosis- conditions where cells under go premature  
 CC cell death as a result of triggers which may or may not be apparent.  
 CC They may also be used in this way to develop cell lines which remain  
 CC viable in culture for an extended period. In contrast, if they act as  
 CC cell death stimulators, Rbcl-y and Hbcl-y may be used to treat  
 CC conditions associated with prolonged cell life span such as cancer  
 CC (especially Kaposi's sarcoma and lung cancer) and auto/hyperimmune  
 CC diseases. They may also be used to cause cell death in, and hence  
 CC control, parasites.  
 CC XX  
 SQ Sequence 192 AA;  
 Query Match 10.0%; Score 148; DB 20; Length 192;  
 Best Local Similarity 24.3%; Pred. No. 2.8e-08;  
 Matches 51; Conservative 30; Mismatches 93; Indels 36; Gaps 8;  
 QY 79 DIEGFVVDYFTHIRONGEMWFGAGLPCGVPEHEMRVWGTTFEKKHAENFEFCOL 138  
 DB 8 DTRALVDEPVGKLRQKGYVCGAGPGCPADPLHQAMRAAGDEFEFRFRFTSDLAOL 67  
 QY 139 LAVP-----RISFSLYQDVVTVGNNAQTDCPSYGRLLIGLSFGFVAAKMM--ES 188

Db 68 HVTGSAQQRFTQVSDLEFG-----GNMGRIVAFVFGALCAESYNKEM 114  
 QY 189 VELGQVNRNLFVYTSLEFKTRIRNNKRNHNSWDPEMTLGKQKEDYERAEKVRGRKQ 248  
 Db 115 EPLVGQVQEMWV---AYLETRLA-DWTHSSGMAEFETAL-----YGDGALDE-ARRLR 162  
 QY 249 NRRWSMIGAGVTAGAIIGVGVVCGRRMFS 278  
 Db 163 EGNMASVVRT-VLTGAVALGALVTGAFEFAS 191

RESULT 9  
 AAM36047  
 ID AAM36047 standard; Protein; 193 AA.

AC AAM36047;  
 DT 22-APR-1998 (first entry)  
 DE Human bcl-2 protein.  
 KM Bcl-2; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;  
 KM diagnosis; degenerative disease.

OS Homo sapiens.  
 PN MO9735971-A1.  
 PD 02-OCT-1997.  
 PE 27-MAR-1997; 97WO-AU00199.  
 PR 27-MAR-1996; 96AU-0008965.

PA (AMRA-) AMRAD OPERATIONS PTY LTD.

PI Adams JM, Cory S, Gibson LM, Holmgren SP;

DR WPI; 1997-489635/45.

DR N-PSDB; AAT96577.

PT Nucleic acid encoding apoptosis related gene bcl-2 - used to induce  
 PT or inhibit cell survival, e.g. for treatment of cancer and  
 PT degenerative diseases

PS Claim 6; Page 48; 86pp; English.

CC This sequence represents a novel human protein, bcl-2, encoded by the  
 CC bcl-2 gene family and extracted from an adult brain library. This gene  
 CC promotes cell survival, so its modulation is useful in treatment of  
 CC cancer or auto-immune diseases, degenerative diseases (e.g. stroke,  
 CC Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,  
 CC ischemia, human immunodeficiency virus infection or in cell transplants.  
 CC up-regulation of the gene can also be used to modify cell lines cultured  
 CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas  
 CC and to increase survival of primary explants during genetic modification.  
 CC It can be used to produce recombinant Bcl-2 for therapy, diagnosis,  
 CC antibody production or screening of potential modulators.

XX Sequence 193 AA;

Query Match 10.0%; Score 148; DB 18; Length 193;

Best Local Similarity 24.3%; Pred. No. 2.9e-08;

Matches 51; Conservative 30; Mismatches 93; Indels 36; Gaps 8;

QY 79 DIEGFVVDYFTIRIRONGMFWGAPGLPGVQPEHEMNRWGTTFEKKHAENFTFCEQL 138

Db 9 DTRALVADFGVTKRQKGYCGAGPEGPADPLHQAMRAAGDEFETFRRTFSDLAQL 68

QY 139 LAVP-----RISFSLYQDVVTRVGNAGTQCPMSYGRLLIGLSFGFVAAKMM--ES 188

Db 69 HVTGSAQQRFTQVSDLEFG-----GNMGRIVAFVFGALCAESYNKEM 115

QY 189 VELGQVNRNLFVYTSLEFKTRIRNNKRNHNSWDPEMTLGKQKEDYERAEKVRGRKQ 248  
 Db 116 EPLVGQVQEMWV---AYLETRLA-DWTHSSGMAEFETAL-----YGDGALDE-ARRLR 163  
 QY 249 NRRWSMIGAGVTAGAIIGVGVVCGRRMFS 278  
 Db 164 EGNMASVVRT-VLTGAVALGALVTGAFEFAS 192

RESULT 10  
 AAM61392  
 ID AAM61392 standard; Protein; 193 AA.

AC AAM61392;  
 DT 02-OCT-1998 (first entry)

DE Human bcl-2 protein.

KM bcl-2; bcl-2; cell death pathway; apoptotic; apoptosis; human.

OS Homo sapiens.

PN US5789201-A.

PD 04-AUG-1998.

PE 11-FEB-1997; 97US-0798897.

PR 23-FEB-1996; 96US-0012201.

PR 11-FEB-1997; 97US-0798897.

PA (COCE-) COCENSYS INC.

PI Guastella J;

DR WPI; 1998-446079/38.

DR N-PSDB; AAV28334.

PT Nucleic acids encoding B-cell lymphoma-2 protein - useful for  
 PT producing recombinant protein for use in treating uncontrolled cell  
 PT growth e.g. cancers

PS Example; Column 17/18; 27pp; English.

CC The mammalian bcl-2 protein is a member of the bcl-2 family, components  
 CC in the cell death pathway. The bcl-2 family have both apoptotic activity  
 CC and the apoptosis blocking activity. bcl-2 fails in the apoptosis  
 CC activity category. The recombinant protein may be used to prevent  
 CC uncontrolled cell growth, either by its direct administration to  
 CC recombinant genetic constructs to increase its expression in vivo. Also,  
 CC antisense constructs can be used in disorders where prevention of cell  
 CC death is desired.

XX Sequence 193 AA;

Query Match 10.0%; Score 148; DB 19; Length 193;

Best Local Similarity 24.3%; Pred. No. 2.9e-08;

Matches 51; Conservative 30; Mismatches 93; Indels 36; Gaps 8;

QY 79 DIEGFVVDYFTIRIRONGMFWGAPGLPGVQPEHEMNRWGTTFEKKHAENFTFCEQL 138

Db 9 DTRALVADFGVTKRQKGYCGAGPEGPADPLHQAMRAAGDEFETFRRTFSDLAQL 68

QY 139 LAVP-----RISFSLYQDVVTRVGNAGTQCPMSYGRLLIGLSFGFVAAKMM--ES 188

Db 69 HVTGSAQQRFTQVSDLEFG-----GNMGRIVAFVFGALCAESYNKEM 115

QY 189 VELGQVNRNLFVYTSLEFKTRIRNNKRNHNSWDPEMTLGKQKEDYERAEKVRGRKQ 248

Db 116 EPLVGQVQEMWV---AYLETRLA-DWTHSSGMAEFETAL-----YGDGALDE-ARRLR 163

QY 249 NRRSMIGAGYTAGAIGIVGVCGRMFMS 278  
 DB 164 EGNWASVRT-VLTGAVALGALVTGAFEPAS 192

## RESULT 11

AAV05532  
 ID AAV05532 standard; Protein; 193 AA.

AC AAV05532;

DT 05-JUL-1999 (first entry)

DE Human Bcl-w protein essential for spermatogenesis.

KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;  
 animal model.

XX Homo sapiens.

XX WO9913710-A1.

XX 25-MAR-1999.

XX 16-SEP-1998; 98WO-AU00764.

XX 16-SEP-1997; 97AU-0009228.

XX (HAL-) HALL INST MEDICAL RES WALTER & ELIZA.

XX Adams J, Cory S, Gibson L, Koenigen F, Print C;

XX WPI; 1999-243890/20.

XX N-PSDB; AAX25134.

XX An animal model exhibiting reduced levels of a Bcl-w protein and/or

XX protein associated with Bcl-w

XX Disclosure; Page 37; 52pp; English.

XX The present sequence is described of a derivative of human Bcl-w  
 (see also AAY05530), a pro-survival member of the Bcl-2 family that  
 is widely expressed and which is essential for spermatogenesis.  
 CC The invention relates generally to a method of treatment and to an  
 CC animal model for the identification of molecules and genetic  
 CC sequences useful for inducing or reducing fertility of male animals.  
 CC Methods are provided for the treatment of infertility, or for  
 CC reducing fertility, by modulating spermatogenesis. An animal model  
 CC carries a mutation is at least one allele of the human or murine  
 CC bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w.  
 CC Such animals have disorganised seminiferous tubules and are  
 CC substantially infertile, but possess no other major abnormalities  
 CC as determined by histological examination. They can be used to  
 CC screen for therapeutic molecules including genetic sequences  
 CC capable of inducing, enhancing or otherwise facilitating  
 CC spermatogenesis in animals, or which can induce infertility.

XX Sequence 193 AA;

XX Query Match 10.0%; Score 148; DB 20; Length 193;

XX Best Local Similarity 24.3%; Pred. No. 2.9e-08;

XX Matches 51; Conservative 30; Mismatches 93; Indels 36; Gaps 8;

QY 79 DIEGVDVYTHIRNONGEMFGARGLPCGVPEHEHMRWGTTEKKHAENFEFFCQL 138

DB 9 DTRALVAVFVGKLRQKGVCGAGCEGPADPLHQARRAGDEFEFRRTFSDLAQL 68

QY 139 LAVP-----RISFSLYODVVRVGNAGOTDCPMYSGRLIGLSFGFVAAKM--ES 188

DB 69 HTYPSAGQORFTQVSDLEFGG-----GPNMGRVLAFLFLGALCAESVKNEM 115

QY 189 VELQGOVRLNFVYTSLEFTRIRNMKKEHNSWDEFTLQGMKDEYERAEAKVGRKK 248

DB 116 EPLVGQVEEMV---AYLETRL-VDMIHSSGMAEFETL-----YGDALAE-ARRLR 163  
 QY 249 NRRSMIGAGYTAGAIGIVGVCGRMFMS 278  
 DB 164 EGNWASVRT-VLTGAVALGALVTGAFEPAS 192

## RESULT 12

AAW97392  
 ID AAW97392 standard; Protein; 193 AA.

AC AAW97392;

DT 20-MAY-1999 (first entry)

DE The human bcl-y protein.

KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
 KW head trauma; Alzheimer's disease; neural; muscular degenerative disease;  
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
 KW premature cell death; cell death stimulator; prolonged cell life span;  
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;  
 KW parasite.

XX Homo sapiens.

XX US5883229-A.

XX 16-MAR-1999.

XX 25-NOV-1997; 97US-0978523.

XX 23-FEB-1996; 96US-0012201.

XX 11-FEB-1997; 97US-0798897.

XX 25-NOV-1997; 97US-0978523.

XX (COCE-) COCENSYS INC.

XX Guastella J;

XX WPI; 1999-214150/18.

XX N-PSDB; AAX15946.

XX Novel bcl-y homologues of the rat and human bcl-2 protein - useful  
 XX for modulating programmed cell death

XX Claim 1; Columns 17-18; 26pp; English.

XX The present sequence represents human bcl-y protein (Hbcl-y). The  
 CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and  
 CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in  
 CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y  
 CC proteins may be used to treat conditions associated with a disruption of  
 CC the cell death pathway. If they act as cell death inhibitors, they may be  
 CC used in therapies to treat subjects suffering from: strokes, head trauma,  
 CC Alzheimer's disease, neural and muscular degenerative diseases  
 CC (especially multiple sclerosis), myocardial infarction, vitally induced  
 CC cell death, aging, spinal cord injuries and amyotrophic lateral  
 CC sclerosis- conditions where cells under go premature cell death as a  
 CC result of triggers which may or may not be apparent. They may also be  
 CC used in this way to develop cell lines which remain viable in culture for  
 CC an extended period. In contrast, if they act as cell death stimulators,  
 CC Rbcl-y and Hbcl-y may be used to treat conditions associated with  
 CC prolonged and bcl-y span such as cancer (especially Kaposi's sarcoma and  
 CC lung cancer) and auto/hyperimmune diseases. They may also be used to  
 CC cause cell death in, and hence control, parasites.

XX Sequence 193 AA;

XX Query Match 10.0%; Score 148; DB 20; Length 193;

XX Best Local Similarity 24.3%; Pred. No. 2.9e-08;

Matches	51;	Conservative	30;	Mismatches	93;	Indels	36;	Gaps	8
OY	79	DIEGIVVDYFTIRIQNGNEMFGAPCLPCGVQPEHEMMVMGTEIFPKKAENFETCEOL	138						
Db	9	DLRALVEDEVYKLRKGKGVCGAGPEGPAADPLHQAAMRAAGDEFTRRRRTFSDIAQL	68						
OY	139	IAPV-----RISPELYQDVVRYTGNATQDCCPMSPYGLIGLISFGGFVAKKM--ES	188						
Db	69	HVTPGSAQGRFLQVSDLELFG-----GNWRILVAFVFGAALCAESYNKEM	115						
OY	169	VELQGVRLLEFYTSLFITRIRNNKKEHNRSDPMTGKQKEDYEAEAEKVRKKQ	248						
Db	116	EPLVQVQVEWMM--AYLETRLA-DWIHSSGMAEFTAL-----YDGALEE-ARRLR	163						
OY	249	NRKSMIGAGYTAGAIGIVGVVCGHMPFS	278						
Db	164	EGNMASVRT-VLTGAVALCALVTVGAFAS	192						
RESULT 13									
AAM36048									
ID	AAM36048	standard; Protein; 168 AA.							
XX	AC	AAM36048;							
XX	DT	22-APR-1998 (first entry)							
XX	DE	Mouse bcl-w protein.							
XX	Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;								
KW	diagnosis; degenerative disease.								
XX	Mus sp.								
XX	PN	W09735971-A1.							
XX	PD	02-OCT-1997.							
XX	PE	27-MAR-1997; 97WO-AU00199.							
XX	PR	27-MAR-1996; 96AU-0008965.							
XX	PA	(AMRA-) AMRAD OPERATIONS PTY LTD.							
PI	Adams JM, Cory S, Gibson LM, Holmgren SP;								
XX	DR	WPI: 1997-489635/45.							
XX	DR	N-PSDB; AAT96578.							
PT	Nucleic acid encoding apoptosis related gene bcl-w - used to induce								
PT	or inhibit cell survival, e.g. for treatment of cancer and								
PT	degenerative diseases								
XX	Claim 6; Page 50-51; 86pp; English.								
XX	This sequence represents a novel protein, bcl-w, encoded by the mouse								
XX	bcl-2 gene family. This gene promotes cell survival, so its modulation								
XX	is useful in treatment of cancer or auto-immune diseases, degenerative								
XX	diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular								
XX	degeneration, hypoxia, ischemia, human immunodeficiency virus infection								
XX	or in cell transplants. Up-regulation of the gene can also be used to								
XX	modify cell lines cultured in vivo, e.g. to develop new lines, to								
XX	facilitate isolation of hybridomas and to increase survival of primary								
XX	cell explants during genetic modification. It can be used to produce								
XX	recombinant Bcl-w for therapy, diagnosis, antibody production or								
XX	screening of potential modulators.								
XX	Sequence 168 AA;								

Sequence	168 AA;
Sequence	168 AA;

Query Match	9.8%;	Score 145.5;	DB 18;	Length 168;
Best Local Similarity	25.8%;	Pred. No. 4.5e-08;		
Matches	48;	Conservative	24;	Mismatches 77;
				Indels 37;
				Gaps 7;






```

QY 79 DIEGVADYFETHIRKONGMEMEGAPGLDGVOPHEHMMRWGTFEKKHAENETFEOL 138
Db 9 DTRALVADYVYRIKROKGYVCAGRGEGCPADPLHOMKRAAGDEFETRFRRTSDLAOL 68
QY 139 LAVP-----RISFSLYODVYRTVGNAOTDCCPMSYGRLLIGLSFGFVAAKM--ES 188
Db 69 HVTGSAQOQRETYQSDLEFG-----GPMWGRLTAVFVFGALCAESYVKEM 115
QY 189 VELOQVQRNLEFYVTSLEIKTRIRNNKKEHNRSDDEFITL--CKQMKEDYERAEAEKVGRRK 247
Db 116 EPLVGVQVODWIV---AVLETRLA-DWIIHSGGWADFTALRGDGED-----ARRL 162
QY 248 QNRRMS 253
Db 163 REGNWA 168

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DB 163 REGNWA 168

RESULT 14

ID	Protein; 233 AA
AAB73304	standard; 233 AA

AC AAB73304;

DT 22-MAY-2001 (first entry)

DE Mutant rat Bcl-XL protein, Bcl-XFNK.

Rat Bcl-XL mutant; Bcl-xFNK; apoptosis inhibitor; membrane permeable;

KW cell death-associated disease; tissue transplant preservative; mutagen

05 Rattus norvegicus.

XX  
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F0030001 1 2007 21

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2  
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XX 17-APR-2000 2000HQ-TD0EE00

XX 17-AUG-1000. 00TD-0230643

XX  
 (INTRO) / TADAN GOT : EMBROIDERY GOOD

XX	
DT	

XX  
FBI - 2001-211210/21

XX  
XX  
Mod: 11/17/2017

PT permeability to enhance uptake for effective inhibition of cell death

PT death  
yy

PS Claim 1; Page 46-47; 56pp; Japanese.  
XX

CC The invention relates to a mutant rat Bcl-x protein and the cdna  
CC encoding it. The mutant rat Bcl-x protein (Bcl-xENK) has the

CC substitutions Y22E, Q26N, and R165K relative to the wild-type Bcl-XL  
CC protein. The invention also encompasses recombinant vectors and host  
CC

cells comprising the modified nucleic acid sequence. The mutant Bcl-X protein is able to permeate the cell membrane, thus enhancing its

CC apoptosis (programmed cell death). Bcl-2 and Bcl-xL are anti-apoptotic proteins that inhibit apoptosis by acting as inhibitors of the Bcl-2 family of proteins. Bcl-2 and Bcl-xL are also involved in the regulation of cell survival and proliferation.

CC in additives for maintaining the stability of transplanted cells and

cc organs; the present sequence represents the mutant rat Bcl-XL protein  
cc Bcl-xFNK.  
cc

XX	Sequence	233	AA:
SO			

Query Match 9.38; Score 138; DB 22; Length 233;

Best Local Similarity	21.38; Fied. NO. 3.3e-07;				
Matches	53; Conservative	39; Mismatches	81; Indels	76; Gaps	10;





100

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OM protein - protein search, using sw model

Run on: February 24, 2003, 11:53:04 ; Search time 14 Seconds  
(without alignments)  
588.458 Million cell updates/sec

Title: US-09-993-420A-3  
Perfect score: 1479  
Sequence: 1 MTRCTADNSLTNPATRRRM.....ACATGIVGVYCGRMFSLK 280

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued-Patents-AA:\*  
1: /cgn2\_6/prodata/1/iaa/3A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfileasl.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1479	100.0	280	1	US-08-471-058-19
2	1479	100.0	280	3	US-08-471-057-19
3	1479	100.0	280	4	US-09-234-186-3
4	1479	100.0	280	4	US-09-233-527-3
5	1479	100.0	280	5	PCT-US93-05651-3
6	156	10.5	27	2	US-08-733-505A-49
7	156	10.5	27	2	US-08-706-741B-84
8	156	10.5	27	2	US-08-924-695A-84
9	151	10.2	192	1	US-08-978-897-5
10	151	10.2	192	1	US-08-978-897-5
11	151	10.2	193	1	US-08-978-897-3
12	151	10.2	193	2	US-08-978-897-3
13	148	10.0	192	1	US-08-978-897-6
14	148	10.0	192	1	US-08-978-897-6
15	148	10.0	193	1	US-08-978-897-4
16	148	10.0	193	2	US-08-978-897-4
17	135.5	9.2	225	4	US-09-101-519-1
18	135	9.1	233	1	US-08-333-565-59
19	135	9.1	233	1	US-08-081-448-6
20	135	9.1	233	1	US-08-607-269-24
21	135	9.1	233	1	US-08-471-058-14
22	135	9.1	233	2	US-08-661-479-59
23	135	9.1	233	2	US-08-470-670A-7
24	135	9.1	233	3	US-08-471-057-14
25	135	9.1	233	3	US-08-481-739-2
26	135	9.1	233	4	US-09-167-921-2
27	135	9.1	233	4	US-09-323-743-2

28	135	9.1	233	4	US-08-461-511A-7	Sequence 7, Appl
29	135	9.1	233	5	PCT-US94-07089-7	Sequence 7, Appl
30	135	9.1	233	5	PCT-US95-04600-24	Sequence 24, Appl
31	132	8.9	233	4	US-09-271-014A-6	Sequence 6, Appl
32	126	8.5	365	4	US-09-149-476-696	Sequence 66, App
33	120.5	8.1	232	2	US-08-408-095-17	Sequence 17, Appl
34	119.5	8.1	232	2	US-08-408-095-18	Sequence 18, Appl
35	118.5	8.0	236	1	US-08-607-269-22	Sequence 22, Appl
36	118.5	8.0	236	4	US-09-127-048-9	Sequence 9, Appl
37	118.5	8.0	236	5	PCT-US95-04600-22	Sequence 22, Appl
38	117	7.9	239	2	US-08-365-486A-17	Sequence 17, Appl
39	117	7.9	239	2	US-08-408-095-16	Sequence 16, Appl
40	117	7.9	239	4	US-08-880-342-17	Sequence 17, Appl
41	116	7.8	233	1	US-08-607-269-23	Sequence 23, Appl
42	116	7.8	233	5	PCT-US95-04600-23	Sequence 23, Appl
43	116	7.8	239	1	US-08-112-208C-10	Sequence 10, Appl
44	116	7.8	239	1	US-08-248-819A-10	Sequence 10, Appl
45	116	7.8	239	1	US-08-607-269-20	Sequence 20, Appl

## ALIGNMENTS

RESULT 1  
US-08-471-058-19  
; Sequence 19, Application US/08471058  
; Patent No. 5770443  
; GENERAL INFORMATION:  
; APPLICANT: Kiefer, Michael C.  
; TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING  
; PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/471,058  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/320,157  
; FILING DATE: 07-OCT-1994  
; APPLICATION NUMBER: 08/160,067  
; FILING DATE: 30-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: lehnhardt, Susan K  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 23647-20007.12  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-813-5600  
; TELEFAX: 415-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ. ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 280 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-471-058-19  
Query Match 100.0%; Score 1479; DB 1; Length 280;  
Best Local Similarity 100.0%; Pred. No. 1.8e-164;

Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADQDLPSRSROASTRRM 60  
 Db 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADQDLPSRSROASTRRM 60

QY 61 SIGESIDKINDMEPRLDIEGFVVDYFTHRIKONGMEMFGAPGLPCGVOPHEHMMRYMG 120  
 Db 61 SIGESIDKINDMEPRLDIEGFVVDYFTHRIKONGMEMFGAPGLPCGVOPHEHMMRYMG 120

QY 121 TIFEKKAENFEFTCEQLLAVPRISFSLYODVYRTVGNADQDCPMSYGRLLIGLSFGGF 180  
 Db 121 TIFEKKAENFEFTCEQLLAVPRISFSLYODVYRTVGNADQDCPMSYGRLLIGLSFGGF 180

QY 181 VAAKMMESVELOGVRLNFVYTSLEFKTRIRNNMKEHNRSDDEPMTLGKQKEDYERAEA 240  
 Db 181 VAAKMMESVELOGVRLNFVYTSLEFKTRIRNNMKEHNRSDDEPMTLGKQKEDYERAEA 240

QY 241 EKVGRKONRRMSMIGAGVTAGATGIVGVVCGRMFSLK 280  
 Db 241 EKVGRKONRRMSMIGAGVTAGATGIVGVVCGRMFSLK 280

## RESULT 2

US-08-471-057-19  
 ; Sequence 19, Application US/08471057  
 ; Patent No. 6015687  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIEFER, MICHAEL C.  
 ; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
 ; NUMBER OF SEQUENCES: 22  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: MORRISON & FOERSTER  
 ; STREET: 755 Page Mill Road  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94304-1018  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/471,057  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/320,157  
 ; FILING DATE: 07-OCT-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: LEHNHARDT, SUSAN K.  
 ; REGISTRATION NUMBER: 33,943  
 ; REFERENCE/DOCKET NUMBER: 23647-20007.20  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 813-5600  
 ; TELEFAX: (415) 494-0792  
 ; TELEX: 706141  
 ; INFORMATION FOR SEQ. ID NO: 19:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 280 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-471-057-19

Query Match 100.0%; Score 1479; DB 3; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-164;  
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADQDLPSRSROASTRRM 60

Db 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADQDLPSRSROASTRRM 60  
 QY 61 SIGESIDKINDMEPRLDIEGFVVDYFTHRIKONGMEMFGAPGLPCGVOPHEHMMRYMG 120  
 Db 61 SIGESIDKINDMEPRLDIEGFVVDYFTHRIKONGMEMFGAPGLPCGVOPHEHMMRYMG 120

QY 121 TIFEKKAENFEFTCEQLLAVPRISFSLYODVYRTVGNADQDCPMSYGRLLIGLSFGGF 180  
 Db 121 TIFEKKAENFEFTCEQLLAVPRISFSLYODVYRTVGNADQDCPMSYGRLLIGLSFGGF 180

QY 181 VAAKMMESVELOGVRLNFVYTSLEFKTRIRNNMKEHNRSDDEPMTLGKQKEDYERAEA 240  
 Db 181 VAAKMMESVELOGVRLNFVYTSLEFKTRIRNNMKEHNRSDDEPMTLGKQKEDYERAEA 240

QY 241 EKVGRKONRRMSMIGAGVTAGATGIVGVVCGRMFSLK 280  
 Db 241 EKVGRKONRRMSMIGAGVTAGATGIVGVVCGRMFSLK 280

## RESULT 3

US-09-234-186-3  
 ; Sequence 3, Application US/09234186  
 ; Patent No. 6312947  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Horvitz, H. Robert  
 ; APPLICANT: Hengartner, Michael  
 ; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A  
 ; FILE REFERENCE: 01997/201005  
 ; CURRENT APPLICATION NUMBER: US/09/234,186  
 ; EARLIER FILING DATE: 1999-01-20  
 ; EARLIER APPLICATION NUMBER: 07/898,933  
 ; EARLIER FILING DATE: 1992-06-12  
 ; EARLIER APPLICATION NUMBER: 07/927,681  
 ; EARLIER FILING DATE: 1992-08-10  
 ; EARLIER APPLICATION NUMBER: 08/288,295  
 ; EARLIER FILING DATE: 1994-08-10  
 ; EARLIER APPLICATION NUMBER: 08/801,248  
 ; EARLIER FILING DATE: 1997-02-19  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 280  
 ; TYPE: PRT  
 ; ORGANISM: Caenorhabditis elegans  
 ; US-09-234-186-3

Query Match 100.0%; Score 1479; DB 4; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-164;  
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADQDLPSRSROASTRRM 60  
 Db 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADQDLPSRSROASTRRM 60

QY 61 SIGESIDKINDMEPRLDIEGFVVDYFTHRIKONGMEMFGAPGLPCGVOPHEHMMRYMG 120  
 Db 61 SIGESIDKINDMEPRLDIEGFVVDYFTHRIKONGMEMFGAPGLPCGVOPHEHMMRYMG 120

QY 121 TIFEKKAENFEFTCEQLLAVPRISFSLYODVYRTVGNADQDCPMSYGRLLIGLSFGGF 180  
 Db 121 TIFEKKAENFEFTCEQLLAVPRISFSLYODVYRTVGNADQDCPMSYGRLLIGLSFGGF 180

QY 181 VAAKMMESVELOGVRLNFVYTSLEFKTRIRNNMKEHNRSDDEPMTLGKQKEDYERAEA 240  
 Db 181 VAAKMMESVELOGVRLNFVYTSLEFKTRIRNNMKEHNRSDDEPMTLGKQKEDYERAEA 240

QY 241 EKVGRKONRRMSMIGAGVTAGATGIVGVVCGRMFSLK 280  
 Db 241 EKVGRKONRRMSMIGAGVTAGATGIVGVVCGRMFSLK 280

## RESULT 4

```

US-09-233-527-3
; Sequence 3, Application US/09233527
; Patent No. 645617
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: 01997/201004
; CURRENT APPLICATION NUMBER: US/09/233,527
; CURRENT FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 07/898,933
; PRIOR FILING DATE: 1992-06-12
; PRIOR APPLICATION NUMBER: 07/927,681
; PRIOR FILING DATE: 1992-08-10
; PRIOR APPLICATION NUMBER: 08/288,295
; PRIOR FILING DATE: 1994-08-10
; PRIOR APPLICATION NUMBER: 08/801,248
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-233-527-3

```

```

Query Match          100.0%; Score 1479; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 1.8e-164;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADQDLPSFSROASTRRM 60
DB 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADQDLPSFSROASTRRM 60
QY 61 SIGESIDKINDWEPRLDIEGFVVDYFTHIRONGMEMFAPGLPCGVOPHEHMMRYMG 120
DB 61 SIGESIDKINDWEPRLDIEGFVVDYFTHIRONGMEMFAPGLPCGVOPHEHMMRYMG 120
QY 121 TFEKKHAENFTFCEQLLAVPRISFLYODVVRTVGNAGTDQCPMSYGRILGLISFGGF 180
DB 121 TFEKKHAENFTFCEQLLAVPRISFLYODVVRTVGNAGTDQCPMSYGRILGLISFGGF 180
QY 181 VAKKMESEVLOGOVNLFVYTSLEFKTRIRNNMKEHNRSMDDEFTLGKOKKEDYERAE 240
DB 181 VAKKMESEVLOGOVNLFVYTSLEFKTRIRNNMKEHNRSMDDEFTLGKOKKEDYERAE 240
QY 241 EKVGRRKORRRSMIGAGVTAGATGIVGVVCGRMFSLK 280
DB 241 EKVGRRKORRRSMIGAGVTAGATGIVGVVCGRMFSLK 280

```

## RESULT 5

```

PCT-US93-05651-3
; Sequence 3, Application PC/TUS9305651
; GENERAL INFORMATION:
; TITLE OF INVENTION: A Gene Which Prevents Programmed Cell Death
; NUMBER OF SEQUENCES: 5
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05651
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-05651-3

```

```

Query Match          100.0%; Score 1479; DB 5; Length 280;
Best Local Similarity 100.0%; Pred. No. 1.8e-164;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADQDLPSFSROASTRRM 60
DB 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADQDLPSFSROASTRRM 60
QY 61 SIGESIDKINDWEPRLDIEGFVVDYFTHIRONGMEMFAPGLPCGVOPHEHMMRYMG 120
DB 61 SIGESIDKINDWEPRLDIEGFVVDYFTHIRONGMEMFAPGLPCGVOPHEHMMRYMG 120
QY 121 TFEKKHAENFTFCEQLLAVPRISFLYODVVRTVGNAGTDQCPMSYGRILGLISFGGF 180
DB 121 TFEKKHAENFTFCEQLLAVPRISFLYODVVRTVGNAGTDQCPMSYGRILGLISFGGF 180
QY 181 VAKKMESEVLOGOVNLFVYTSLEFKTRIRNNMKEHNRSMDDEFTLGKOKKEDYERAE 240
DB 181 VAKKMESEVLOGOVNLFVYTSLEFKTRIRNNMKEHNRSMDDEFTLGKOKKEDYERAE 240
QY 241 EKVGRRKORRRSMIGAGVTAGATGIVGVVCGRMFSLK 280
DB 241 EKVGRRKORRRSMIGAGVTAGATGIVGVVCGRMFSLK 280

```

## RESULT 6

```

US-08-733-505A-49
; Sequence 49, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-49

```

```

Query Match          10.5%; Score 156; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.9e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 73 WEPRLDIEGFVVDYFTHIRONGMEW 99
DB 1 WEPRLDIEGFVVDYFTHIRONGMEW 27

```

RESULT 7  
US-08-706-741B-84  
Sequence 84, Application US/08706741B  
Patent No. 5935593  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, STANLEY J.  
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BLVD., SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: USA  
ZIP: 63146  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/706,741B  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 965017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-706-741B-84

Query Match 10.5%; Score 156; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.9e-11;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 WEPRLDIEGFVVDYFTHIRONGMEW 99  
DB 1 WEPRLDIEGFVVDYFTHIRONGMEW 27

RESULT 8  
US-08-924-695A-84  
Sequence 84, Application US/08924695A  
Patent No. 5998583  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, STANLEY J.  
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BLVD., SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: USA  
ZIP: 63105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/924,695A

FILING DATE: 09-SEP-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 971798  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-924-695A-84

Query Match 10.5%; Score 156; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.9e-11;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 WEPRLDIEGFVVDYFTHIRONGMEW 99  
DB 1 WEPRLDIEGFVVDYFTHIRONGMEW 27

RESULT 9  
US-08-798-897-5  
Sequence 5, Application US/08798897  
Patent No. 5789201  
GENERAL INFORMATION:  
APPLICANT: Gastella, John  
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 192 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-798-897-5

Query Match 10.2%; Score 151; DB 1; Length 192;  
Best Local Similarity 24.3%; Pred. No. 1.7e-09;  
Matches 51; Conservative 31; Mismatches 92; Indels 36; Gaps 8;

QY 79 DICEFVVDYFTHIRONGMEWPGALPGVDPFHEHMMRVKGTIFKKHAENFETCEOL 138

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Db      8 DTRALVADFEVGYKLRQKGYVCGAGPEGPAADPLHQAAMRAAGDEFTFRRTFSDLAOL 67
QY      139 LAMP-----RISFSLYODVVRTYGNMOTDCCPMYSYGRLLIGLISFGFVAAKMM--ES 188
Db      68 HVTFGSAQQRFTQVSDLEFG-----GPNMGRVAFVFGAALCAESVNKEM 114
QY      189 VELQGOVNLFPVYTSLEFKTRIRNNMKEHNRSMDDFMTLGKOMKEDYERAEKVGRRQ 248
Db      115 EPLVGQVODMWV---TYLETRLA-DWIHSSGMAEFTAL-----YGDGALBE-ARRLR 162
QY      249 NRRWSMIGAGVTAGAGIIVGVVCGRRMFS 278
Db      163 EGNWASVRT-VLTGAVALGALVTVGAFPAS 191

```

```

RESULT 10
US-08-978-523-5
; Sequence 5, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978, 523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798, 897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483, 0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-978-523-5

```

```

Query Match      10.2% Score 151; DB 2; Length 192;
Best Local Similarity 24.3%; Pred. No. 1.7e-09;
Matches 51; Conservative 31; Mismatches 92; Indels 36; Gaps 8;
QY      79 DIEGFVVDYFTHRIQNGEMWFGAPGLPCGVOPHEHMMRWMTTFEKKHAENFTFCEOL 138
Db      8 DTRALVADFEVGYKLRQKGYVCGAGPEGPAADPLHQAAMRAAGDEFTFRRTFSDLAOL 67
QY      139 LAMP-----RISFSLYODVVRTYGNMOTDCCPMYSYGRLLIGLISFGFVAAKMM--ES 188
Db      68 HVTFGSAQQRFTQVSDLEFG-----GPNMGRVAFVFGAALCAESVNKEM 114

```

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QY      189 VELQGOVNLFPVYTSLEFKTRIRNNMKEHNRSMDDFMTLGKOMKEDYERAEKVGRRQ 248
Db      115 EPLVGQVODMWV---TYLETRLA-DWIHSSGMAEFTAL-----YGDGALBE-ARRLR 162
QY      249 NRRWSMIGAGVTAGAGIIVGVVCGRRMFS 278
Db      163 EGNWASVRT-VLTGAVALGALVTVGAFPAS 191

```

```

RESULT 11
US-08-798-897-3
; Sequence 3, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798, 897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483, 0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-798-897-3

```

```

Query Match      10.2% Score 151; DB 1; Length 193;
Best Local Similarity 24.3%; Pred. No. 1.7e-09;
Matches 51; Conservative 31; Mismatches 92; Indels 36; Gaps 8;
QY      79 DIEGFVVDYFTHRIQNGEMWFGAPGLPCGVOPHEHMMRWMTTFEKKHAENFTFCEOL 138
Db      9 DTRALVADFEVGYKLRQKGYVCGAGPEGPAADPLHQAAMRAAGDEFTFRRTFSDLAOL 68
QY      139 LAMP-----RISFSLYODVVRTYGNMOTDCCPMYSYGRLLIGLISFGFVAAKMM--ES 188
Db      69 HVTFGSAQQRFTQVSDLEFG-----GPNMGRVAFVFGAALCAESVNKEM 115
QY      189 VELQGOVNLFPVYTSLEFKTRIRNNMKEHNRSMDDFMTLGKOMKEDYERAEKVGRRQ 248
Db      116 EPLVGQVODMWV---TYLETRLA-DWIHSSGMAEFTAL-----YGDGALBE-ARRLR 163
QY      249 NRRWSMIGAGVTAGAGIIVGVVCGRRMFS 278
Db      164 EGNWASVRT-VLTGAVALGALVTVGAFPAS 192

```

```

RESULT 12
US-08-978-523-3

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-798-897-6

Query Match          10.0%; Score 148; DB 1; Length 192;
Best Local Similarity 24.3%; Pred. No. 3.8e-09;
Matches 51; Conservative 30; Mismatches 93; Indels 36; Gaps 8;

QY 79 DIEGVVYFTHRIQNQNMENWGAGLFCGVPHEHMRWMTSTIEKKHAENFEFFCQL 138
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 8 DTRALVEDFVGKLEKQKYVCGAGGEGSPADPLHQAKRAGDEFEFRFRFFSDLAQL 67
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 139 LAVP-----RISFSIQDVVFRTVGNAGTDCPMYSYGRLLIGLISFCGFVAKKM--ES 188
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 68 HTVPESAQQRFTQVSDLEFG-----GPNMGRIVAFVFYFCAALCAESVKNEM 114
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 189 VELGQVNLVYVYSLFKTRIRNNKKEHNSWDDEMTLIGQMKEDYERABAEKVGRRKQ 248
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 115 EPLVGQVOENVV--AYLETRLA-DWHSISGMAEFAL-----YGDALGE-ARRLR 162
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 249 NRRWSMIGAGVTAGIGIVGVCGRRMFS 278
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 163 EGNMASVAT-VLTGAVALGALVYGAFFAS 191
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RESULT 14
US-08-978-523-6
; Sequence 6, Application US/08978523
; Patent No. 5883229
;
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-978-523-6

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Query Match 10.0%; Score 148; DB 2; Length 192;

Best Local Similarity 24.3%; Pred. No. 3.8e-09; Matches 51; Conservative 30; Mismatches 93; Indels 36; Gaps 8;

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QY 79 DIEGFVVDYFTHIRIRONGMFMGAPGLPCGVOPHEHMRVMGTTFEKKHAENFETCEOL 138
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Db 8 DTRALVEDEVGYKLRQKGYCGAGPGEPADPLHQAMRAAGDEFETFRRTFSDLAOL 67
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 139 LAVP-----RISFSLYQDVVTVGNAGTDCPMYSYGRLLIGLISFGFVAAKMM--ES 188
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 68 HVTGSAQGRFTQVSDLEFG-----GPNMGRLVAFVFGAALCAESVKNEM 114
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 189 VELQGVNRLFYVTSLEFKTRIRNNMKEHNRSMDDFMTLGKOMKEDYERAERKVGRRKQ 248
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Db 115 EPLVGQVQEMWV---AYLETRLA-DWIHSSGMAEFTAL-----YDGLALEE-ARRLR 162
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QY 249 NRRMSMIGAGVTAGATIGVGVVCGRRMFS 278
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Db 163 EGNMASVRT-VLTGAVALGALVTGAFASF 191
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RESULT 15  
US-08-798-897-4  
Sequence 4, Application US/08798897  
Patent No. 5789201

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; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; City: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.

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; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-798-897-4

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Query Match 10.0%; Score 148; DB 1; Length 193;

Best Local Similarity 24.3%; Pred. No. 3.8e-09; Matches 51; Conservative 30; Mismatches 93; Indels 36; Gaps 8;

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QY 79 DIEGFVVDYFTHIRIRONGMFMGAPGLPCGVOPHEHMRVMGTTFEKKHAENFETCEOL 138
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Db 9 DTRALVEDEVGYKLRQKGYCGAGPGEPADPLHQAMRAAGDEFETFRRTFSDLAOL 68
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QY 139 LAVP-----RISFSLYQDVVTVGNAGTDCPMYSYGRLLIGLISFGFVAAKMM--ES 188
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Db 69 HVTGSAQGRFTQVSDLEFG-----GPNMGRLVAFVFGAALCAESVKNEM 115
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QY 189 VELQGVNRLFYVTSLEFKTRIRNNMKEHNRSMDDFMTLGKOMKEDYERAERKVGRRKQ 248
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Db 116 EPLVGQVQEMWV---AYLETRLA-DWIHSSGMAEFTAL-----YDGLALEE-ARRLR 163
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QY 249 NRRMSMIGAGVTAGATIGVGVVCGRRMFS 278
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Db 164 EGNMASVRT-VLTGAVALGALVTGAFASF 192
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Search completed: February 24, 2003, 11:55:26  
Job time : 15 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 24, 2003, 11:54:44 ; Search time 13 seconds  
(Without alignments)  
669.196 Million cell updates/sec

Title: US-09-993-420A-3

Perfect score: 1479  
Sequence: 1 MTRCTADNSLTNPAYRRRTM.....AGALIGVGVVCGRMFSLK 280

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubppaa/PCF\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB.pep:\*
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- 7: /cgn2\_6/ptodata/1/pubppaa/PCFUS\_PUBCOMB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB.pep:\*
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- 12: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1479	100.0	280	US-10-101-482-19	Sequence 19, Appl
2	154	10.4	193	US-09-925-674A-9	Sequence 9, Appl
3	150	10.1	193	US-09-925-674A-7	Sequence 7, Appl
4	135	9.1	233	US-10-101-482-14	Sequence 14, Appl
5	135	9.1	233	US-09-734-846-2	Sequence 2, Appl
6	135	9.1	233	US-09-952-278-6	Sequence 6, Appl
7	132	8.9	152	US-10-158-769-2	Sequence 1, Appl
8	122.5	8.3	155	US-10-158-769-1	Sequence 12, Appl
9	116	7.8	239	US-10-101-482-12	Sequence 5, Appl
10	114	7.7	239	US-08-726-211-5	Sequence 40954, A
11	99	6.7	235	US-09-864-761-40954	Sequence 2, Appl
12	96	6.5	185	US-10-208-155-2	Sequence 15, Appl
13	95	6.4	226	US-10-101-482-15	Sequence 7, Appl
14	90.5	6.1	205	US-08-726-211-7	Sequence 4, Appl
15	90.5	6.1	205	US-09-952-278-4	Sequence 306, App
16	90	6.1	274	US-09-741-669-106	Sequence 2, Appl
17	89	6.0	190	US-09-952-278-2	Sequence 55, Appl
18	83	5.6	444	US-09-464-099A-55	Sequence 55, Appl
19	83	5.6	444	US-09-861-696-55	Sequence 55, Appl

20	82.5	5.6	447	9	US-09-843-250-23	Sequence 23, Appl
21	82	5.5	1814	10	US-09-920-552-103	Sequence 103, App
22	82	5.5	4342	10	US-09-815-242-5107	Sequence 5107, Ap
23	81.5	5.5	444	9	US-09-464-099A-53	Sequence 53, Appl
24	81.5	5.5	444	10	US-09-861-696-53	Sequence 158, App
25	80.5	5.4	471	10	US-09-765-272-158	Sequence 6, Appl
26	80	5.4	539	10	US-09-935-145-6	Sequence 1329, App
27	80	5.4	558	10	US-09-925-301-1329	Sequence 4, Appl
28	80	5.4	623	10	US-09-862-007-4	Sequence 4, Appl
29	80	5.4	1332	10	US-09-982-091A-4	Sequence 4, Appl
30	79.5	5.4	372	10	US-09-815-242-11156	Sequence 11156, A
31	79.5	5.4	649	10	US-09-815-242-13206	Sequence 13206, A
32	79.5	5.4	650	10	US-09-815-242-13206	Sequence 13667, A
33	79.5	5.4	1701	9	US-09-963-959-2	Sequence 2, Appl
34	78.5	5.3	444	9	US-09-464-099A-54	Sequence 54, Appl
35	78.5	5.3	444	10	US-09-861-696-54	Sequence 54, Appl
36	78.5	5.3	543	9	US-09-738-626-5237	Sequence 5237, Ap
37	78	5.3	172	9	US-10-101-482-16	Sequence 16, Appl
38	78	5.3	441	10	US-09-970-711-26	Sequence 26, Appl
39	78	5.3	445	9	US-10-076-622-473	Sequence 473, App
40	78	5.3	445	10	US-09-825-301-29	Sequence 29, Appl
41	78	5.3	445	10	US-09-604-287A-473	Sequence 473, App
42	78	5.3	445	12	US-10-007-805-473	Sequence 20, Appl
43	78	5.3	449	9	US-09-843-250-20	Sequence 565, App
44	78	5.3	1341	9	US-10-076-622-565	Sequence 565, App
45	78	5.3	1341	12	US-10-007-805-565	Sequence 565, App

## ALIGNMENTS

RESULT 1  
US-10-101-482-19  
Sequence 19, Application US/10101482  
Publication NO. US2003000837A1

GENERAL INFORMATION:  
APPLICANT: KIEFER, MICHAEL C.  
BARR, PHILIP J.  
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
City: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/101,482  
FILING DATE: 18-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/320,157  
FILING DATE: 07-OCT-1994

ATTORNEY/AGENT INFORMATION:  
NAME: LEHNHARDT, SUSAN K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 23647-20007.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141

INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 280 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 19;  
US-10-101-482-19

Query Match 100.0%; Score 1479; DB 9; Length 280;  
Best Local Similarity 100.0%; Pred. No. 3.8e-149;  
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLIGKTEPTDFGINSADADLPSPSRQASTRRM 60  
DB 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLIGKTEPTDFGINSADADLPSPSRQASTRRM 60  
QY 61 SIGESIDGKINDMEEPRLDEGVVDFTFIRIRONGMEMFGAGLPCGVQPEHEMRKRVNG 120  
DB 61 SIGESIDGKINDMEEPRLDEGVVDFTFIRIRONGMEMFGAGLPCGVQPEHEMRKRVNG 120  
QY 121 TIEFKHAENFEFCEOLLAVPRISFLYODVVRVGNADQCPMSYGRLLIGLISFGGF 180  
DB 121 TIEFKHAENFEFCEOLLAVPRISFLYODVVRVGNADQCPMSYGRLLIGLISFGGF 180  
QY 181 VAAKMSVELOGOVRLFYVTSLEFKTRIRNNWKEHNSWDPMTLGKOMKEDYERAE 240  
DB 181 VAAKMSVELOGOVRLFYVTSLEFKTRIRNNWKEHNSWDPMTLGKOMKEDYERAE 240  
QY 241 EKVGRKRRNRRMSMIGAGVTAGAGIYGVVCGRRMFSLK 280  
DB 241 EKVGRKRRNRRMSMIGAGVTAGAGIYGVVCGRRMFSLK 280

RESULT 2  
US-09-925-674A-9  
Sequence 9, Application US/09925674A  
Patent No. US20020119943A1  
GENERAL INFORMATION:  
APPLICANT: AMRAD Operations Pty Ltd  
TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2  
FILE REFERENCE: 11686a  
CURRENT APPLICATION NUMBER: US/09/925,674A  
CURRENT FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 09/925,674  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: PN8965  
PRIOR FILING DATE: 1996-03-27  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 193  
TYPE: PRT  
ORGANISM: Mouse  
US-09-925-674A-9

Query Match 10.4%; Score 154; DB 10; Length 193;  
Best Local Similarity 24.8%; Pred. No. 9.9e-09;  
Matches 52; Conservative 30; Mismatches 92; Indels 36; Gaps 8;

QY 79 DIEGFVVDFTFIRIRONGMEMFGAGLPCGVQPEHEMRKRVNGTIEFKHAENFEFCEOL 138  
DB 9 DTRALVADFTVGRKQKGYVCGAGPGRADPLHQAARAGDEFETRRFRFTSDLAQL 68  
QY 139 LAVP-----RISFSLYODVVRVGNADQCPMSYGRLLIGLISFGGFVAAKMM--ES 188  
DB 69 HTVPGSAOQRFQVSDLELFG-----GPNMGRVAFVFGALCAESVKNEM 115  
QY 189 VELGGOVRLFYVTSLEFKTRIRNNWKEHNSWDPMTLGKOMKEDYERAEKVGRKQ 248  
DB 116 EPLVGQVDMV---AYLETRLA-DWISSGGMAEFAL-----YDGALEE-ARRLR 163  
QY 249 NRRMSMIGAGVTAGAGIYGVVCGRRMFS 278  
DB 164 EGNMASVRT-VLTGAVVALGALVTYGAFFAS 192

RESULT 3  
US-09-925-674A-7  
Sequence 7, Application US/09925674A  
Patent No. US20020119943A1  
GENERAL INFORMATION:  
APPLICANT: AMRAD Operations Pty Ltd  
TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2  
FILE REFERENCE: 11686a  
CURRENT APPLICATION NUMBER: US/09/925,674A  
CURRENT FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 09/925,674  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: PN8965  
PRIOR FILING DATE: 1996-03-27  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 193  
TYPE: PRT  
ORGANISM: HUMAN  
US-09-925-674A-7

Query Match 10.1%; Score 150; DB 10; Length 193;  
Best Local Similarity 24.3%; Pred. No. 2.0e-08;  
Matches 51; Conservative 30; Mismatches 93; Indels 36; Gaps 8;

QY 79 DIEGFVVDFTFIRIRONGMEMFGAGLPCGVQPEHEMRKRVNGTIEFKHAENFEFCEOL 138  
DB 9 DTRALVADFTVGRKQKGYVCGAGPGRADPLHQAARAGDEFETRRFRFTSDLAQL 68  
QY 139 LAVP-----RISFSLYODVVRVGNADQCPMSYGRLLIGLISFGGFVAAKMM--ES 188  
DB 69 HTVPGSAOQRFQVSDLELFG-----GPNMGRVAFVFGALCAESVKNEM 115  
QY 189 VELGGOVRLFYVTSLEFKTRIRNNWKEHNSWDPMTLGKOMKEDYERAEKVGRKQ 248  
DB 116 EPLVGQVDMV---AYLETRLA-DWISSGGMAEFAL-----YDGALEE-ARRLR 163  
QY 249 NRRMSMIGAGVTAGAGIYGVVCGRRMFS 278  
DB 164 EGNMASVRT-VLTGAVVALGALVTYGAFFAS 192

RESULT 4  
US-10-101-482-14  
Sequence 14, Application US/10101482  
Patent No. US20030008837A1  
GENERAL INFORMATION:  
APPLICANT: KIEFER, MICHAEL C.  
BARR, PHILIP J.  
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
ENCODING THE PROTEINS AND METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSER: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/101,482  
FILING DATE: 18-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/320,157  
FILING DATE: 07-Oct-1994



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Db      9 VVDPLSYKLSOKGYSWQSDVEENRTAPECTESEMETPSAINGNPSMHLADSPAVNGA 68
QY      115 -----MMRVMTGLEKKHAENFETPCQQLAVPRISFSLYQDVYR 154
Db      69 TAHSSSLDAREVITPAKAKQALREAGDEFLRYRAFSDDLISQHLITPGTAYQSEQVYN 128
QY      155 TVGNMOTQCPMSYRLLIGLISFGFVAAKMMESV--ELQGVNRLFYVTSLEFKTRIRN 212
Db      129 -----ELFRDGVNMGRIYAFSFGG---ALCVESYKREMOQLVSRIAMMATYLNDEL-E 179
QY      213 NMKEHNSMDPEMTLGKQMKEDY--ERAEAEVGRKKONRKRSMIGAGVTAGATIGVYV 271
Db      180 PMIQNGSGMDTFVEL-----YGNMAAESRKQGERNRWFLTG-----MTVAGVVL 225
QY      272 CGRMFSLK 280
Db      226 LG-SLFSRK 233

RESULT 7
US-10-158-769-2
; Sequence 2, Application US/10158769
; Publication No. US20030008924A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Shaomeng
; TITLE OF INVENTION: Small Molecule Antagonists of BCL-2 Family Protein
; FILE REFERENCE: UM-07232
; CURRENT APPLICATION NUMBER: US/10/158,769
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/293,983
; PRIOR FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-158-769-2

Query Match      8.9%; Score 132; DB 9; Length 152;
Best Local Similarity 24.5%; Pred. No. 1.5e-06;
Matches 38; Conservative 31; Mismatches 66; Indels 20; Gaps 6;

QY      84 VVDYFTHIRIRONGMWF-----GAPGLPCGYQPE--HEMRVMGNIPEKHAENFET 134
Db      5 VVDPLSYKLSOKGYSWQSDVEENRTAPECTESEMETPSAINGNPSMHLADSPAVNGA 68
QY      135 CEQLLAVPRISFSLYQDVYRTVGNMOTQCPMSYRLLIGLISFGFVAAKMMESV--ELQ 192
Db      65 TSQHLITPGTAYQSEQVYN-----ELFRDGVNMGRIYAFSFGG---ALCVESYKREMO 116
QY      193 GOVNRNLFVYVTSLEFKTRIRNMMKEHNSMDPEMTL 227
Db      117 VVVSRIAMMATYLNDEL-EPWIQNGSGMDTFVEL 150

RESULT 8
US-10-158-769-1
; Sequence 1, Application US/10158769
; Publication No. US20030008924A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Shaomeng
; TITLE OF INVENTION: Small Molecule Antagonists of BCL-2 Family Protein
; FILE REFERENCE: UM-07232
; CURRENT APPLICATION NUMBER: US/10/158,769
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/293,983
; PRIOR FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 3

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-158-769-1

Query Match      8.3%; Score 122.5; DB 9; Length 155;
Best Local Similarity 22.8%; Pred. No. 1.6e-05;
Matches 36; Conservative 32; Mismatches 67; Indels 23; Gaps 5;

QY      84 VVDYFTHIRIRONGMWF-----AGPLPCGYQPEHEMRVMGNIPEKHAENF 131
Db      5 VVDPLSYKLSOKGYSWQSDVEENRTAPECTESEMETPSAINGNPSMHLADSPAVNGA 68
QY      132 ETPCEQLLAVPRISFSLYQDVYRTVGNMOTQCPMSYRLLIGLISFGFVAAKMMESV-- 189
Db      65 AEMSRQLHLPTFARGRAFTVE-----ELFRDGVNMGRIYAFSFGGVMC---VESYNR 116
QY      190 ELQGVNRLFYVTSLEFKTRIRNMMKEHNSMDPEMTL 227
Db      117 EMSPIVDNIALMWTXYLNRL-HTWIQNGSGMDAFVEL 153

RESULT 9
US-10-101-482-12
; Sequence 12, Application US/10101482
; Publication No. US20030008837A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; BARB, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FORSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/101,482
; FILING DATE: 18-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-101-482-12

Query Match      7.8%; Score 116; DB 9; Length 239;

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Best Local Similarity 19.4%; Pred. No. 0.00015;  
Matches 48; Conservative 39; Mismatches 76; Indels 84; Gaps 10;

QY 79 DIEGFVVDYFTHIRONGEMWF-----100  
| : : : : :  
Db 10 DNREIWKYIHYKLSQGYENDAGDVGAAPGAPGIFSSQGHHTPHASNDPVART 69  
QY 101 -----GAPGLPG-----VOP-EHEMMRWGTIFEEKHAENFTFCEOLLAVPRISFL 148  
| : : : : :  
Db 70 SPLQTPAPGAAGPALSPVPVHLTLROAGDDFSRRYRDFAFMSROLHLTPPTARGR 129  
QY 149 YQDVVRYVGNAGTQDCPMSYGRLLGLISFGGFVAAKMMESV--ELQGVNRLFYVTSLEFI 206  
| : : : : :  
Db 130 FATVE-----ELFRDGVNMGRIVAFFEEFGVWC---VESVNRMSPLVDNALMTETYL 181  
QY 207 KTRIRNMKEHNRSMDDEFTL-GKQMKEDYERAEAEKVRKKQNRW-----SMIG 256  
| : : : : :  
Db 182 NRHL-HTWIODNGMDAFVELYGPSMRPLDPS-----WLSKTLTLLSLALVG 227

QY 257 AGVTAGA 263  
| : : : : :  
Db 228 ACITLGA 234

RESULT 10  
US-08-726-211-5  
; Sequence 5, Application US/08726211  
; Publication No. US20030012812A1  
; GENERAL INFORMATION:  
; APPLICANT: Torno, Mar  
; APPLICANT: Tarl, Ana M.  
; APPLICANT: Lopez-Berestein, Gabriel  
; TITLE OF INVENTION: INHIBITION OF Bcl-2 PROTEIN EXPRESSION BY  
; TITLE OF INVENTION: LIPOSOMAL ANTISENSE OLIGODEOXYNUCLEOTIDES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/726,211  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wilson, Mark B.  
; REGISTRATION NUMBER: 37,259  
; REFERENCE/DOCKET NUMBER: UTXC:504  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 239 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-726-211-5

Query Match 7.7%; Score 114; DB 1; Length 239;  
Best Local Similarity 19.4%; Pred. No. 0.00024;  
Matches 48; Conservative 39; Mismatches 76; Indels 84; Gaps 10;

QY 79 DIEGFVVDYFTHIRONGEMWF-----100  
| : : : : :  
Db 10 DNREIWKYIHYKLSQGYENDAGDVGAAPGAPGIFSSQGHHTPHASNDPVART 69

QY 101 -----GAPGLPG-----VOP-EHEMMRWGTIFEEKHAENFTFCEOLLAVPRISFL 148  
| : : : : :  
Db 70 SPLQTPAPGAAGPALSPVPVHLTLROAGDDFSRRYRDFAFMSROLHLTPPTARGR 129  
QY 149 YQDVVRYVGNAGTQDCPMSYGRLLGLISFGGFVAAKMMESV--ELQGVNRLFYVTSLEFI 206  
| : : : : :  
Db 130 FATVE-----ELFRDGVNMGRIVAFFEEFGVWC---VESVNRMSPLVDNALMTETYL 181  
QY 207 KTRIRNMKEHNRSMDDEFTL-GKQMKEDYERAEAEKVRKKQNRW-----SMIG 256  
| : : : : :  
Db 182 NRHL-HTWIODNGMDAFVELYGPSMRPLDPS-----WLSKTLTLLSLALVG 227

QY 257 AGVTAGA 263  
| : : : : :  
Db 228 ACITLGA 234

RESULT 11  
US-09-864-761-40954  
; Sequence 40954, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO  
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aeomlca-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 40954  
; LENGTH: 185  
; TYPE: PRT

[illegible]

Query Match 6.48; Score 95; DB 9; Length 226;



Best Local Similarity 25.2%; Pred. No. 0.023;  
Matches 31; Conservative 26; Mismatches 36; Indels 30; Gaps 7;

QY 108 GYQPEHEMAYMGTFE---KHAENEFTEFCQDLAVPRISLSLYQDVYRTVGNATQDQ 163  
DB 95 GYQRNHE---TVFCQMLRKIDIKNE---DVKSLSRMHVFSQDV-----134  
QY 164 CPMSYGRLLISFGFVAKMSEVLEQGVNLF-VYTSLETKIRIRNNKHEHNSMD 222  
DB 135 --TNMGIVTLISFGAFV-AKHKTINQESCIPLEASTIDLVKRT--KRDWLKQKQMD 189  
QY 223 DFM 225  
DB 190 GFV 192

## RESULT 14

US-08-726-211-7  
; Sequence 7, Application US/08726211  
; Publication No. US20030012612A1  
; GENERAL INFORMATION:  
; APPLICANT: Tormo, Mar  
; APPLICANT: Tari, Ana M.  
; TITLE OF INVENTION: INHIBITION OF Bcl-2 PROTEIN EXPRESSION BY  
; NUMBER OF INVENTIONS: LIPOSOMAL ANTISENSE OLIGODEOXYNUCLEOTIDES  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/726,211  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wilson, Mark B.  
; REGISTRATION NUMBER: 37,259  
; REFERENCE/DOCKET NUMBER: UTXC:504  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 205 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-726-211-7

Query Match 6.1%; Score 90.5; DB 1; Length 205;  
Best Local Similarity 19.0%; Pred. No. 0.06;  
Matches 37; Conservative 30; Mismatches 67; Indels 61; Gaps 7;

QY 79 DIEGVVYDTHIRIRONGEMF-----100  
DB 10 DNRREIVMKYIHYKLSQRYEMDAGVGAAPGAPAPGIFSSQPGHTPHPAASRDVPART 69  
QY 101 -----GAGGLPCG-----VQP-EHEMMRYMGTFEKKHAENEFTEFCQDLAVPRISLSL 148  
DB 70 SPLQTPAAPGAAGAPALSPVPVHLLRQAGDDFSRRYRGDFAMSSQLHLTPFTAGR 129  
QY 149 YQDVYRTVGNATQDCPMSYGRLLISFGFVAKMSEV--ELQGVNLFVYTSLEFI 206  
DB 130 FATVVE-----ELFRDGVNMGRIVAFPEFGVVC--VESVNRKMSPLVDNALMTETYL 181

QY 207 KTRIRNNKHEHNSW 221  
DB 182 NRHL-HTWIDNGW 195

## RESULT 15

US-09-952-278-4  
; Sequence 4, Application US/09952278  
; Patent No. US20020137182A1  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Craig B.  
; ADDRESSEE: Lawrence H.  
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:  
; COMPOSITIONS and Methods  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 321 No. US20020137182A1th Clark Street, Suite 800  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60610  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/952,278  
; FILING DATE: 12-Sep-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/081,448  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. US20020137182A1thrup, Thomas E.  
; REGISTRATION NUMBER: 33,268  
; REFERENCE/DOCKET NUMBER: ARCD090  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-744-0090  
; TELEFAX: 312-755-4489  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 205 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-952-278-4

Query Match 6.1%; Score 90.5; DB 10; Length 205;  
Best Local Similarity 19.0%; Pred. No. 0.06;  
Matches 37; Conservative 30; Mismatches 67; Indels 61; Gaps 7;

QY 79 DIEGVVYDTHIRIRONGEMF-----100  
DB 10 DNRREIVMKYIHYKLSQRYEMDAGVGAAPGAPAPGIFSSQPGHTPHPAASRDVPART 69  
QY 101 -----GAGGLPCG-----VQP-EHEMMRYMGTFEKKHAENEFTEFCQDLAVPRISLSL 148  
DB 70 SPLQTPAAPGAAGAPALSPVPVHLLRQAGDDFSRRYRGDFAMSSQLHLTPFTAGR 129  
QY 149 YQDVYRTVGNATQDCPMSYGRLLISFGFVAKMSEV--ELQGVNLFVYTSLEFI 206  
DB 130 FATVVE-----ELFRDGVNMGRIVAFPEFGVVC--VESVNRKMSPLVDNALMTETYL 181  
QY 207 KTRIRNNKHEHNSW 221  
DB 182 NRHL-HTWIDNGW 195

Fri Feb 28 15:49:17 2003

us-09-993-420a-3.rapb

Page 8

Search completed: February 24, 2003, 11:59:22  
Job time : 13 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 24, 2003, 11:53:49 ; Search time 144 Seconds  
(without alignments)  
1253.648 Million cell updates/sec

Title: US-09-993-420A-3  
Perfect score: 1479  
Sequence: 1 MTRCTADNSLTNPAYRRRTM.....AGAGICGVVCGRMFSLK 280

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Pending\_Patents\_AA\_Main:\*  
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4: /cgn2\_6/ptodata/1/paa/US08\_COMB.pep:\*  
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27: /cgn2\_6/ptodata/1/paa/US10\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1479	100.0	280	US-07-927-681-3	Sequence 3, Appli
2	1479	100.0	280	US-08-288-295-3	Sequence 3, Appli
3	1479	100.0	280	US-08-320-157-19	Sequence 19, Appli
4	1479	100.0	280	US-08-470-865-19	Sequence 19, Appli
5	1479	100.0	280	US-08-801-248-3	Sequence 3, Appli
6	1479	100.0	280	US-09-633-200-19	Sequence 19, Appli

7	1479	100.0	280	US-09-791-537-10912	Sequence 10912, A
8	1479	100.0	280	US-09-993-420A-3	Sequence 3, Appli
9	1479	100.0	280	US-10-101-482-19	Sequence 19, Appli
10	1479	100.0	280	US-09-508-745-8	Sequence 8, Appli
11	1479	100.0	280	US-09-155-327B-9	Sequence 9, Appli
12	1479	100.0	280	US-09-155-327B-9	Sequence 84, Appli
13	1479	100.0	280	US-08-706-741A-84	Sequence 84, Appli
14	1479	100.0	280	US-08-706-741A-84	Sequence 84, Appli
15	1479	100.0	280	US-08-733-505-8	Sequence 49, Appli
16	1479	100.0	280	US-08-924-695-84	Sequence 84, Appli
17	1479	100.0	280	US-08-924-695-84	Sequence 24, Appli
18	1479	100.0	280	US-10-071-174-24	Sequence 24, Appli
19	1479	100.0	280	US-09-155-327B-9	Sequence 9, Appli
20	1479	100.0	280	US-09-925-674A-9	Sequence 9, Appli
21	1479	100.0	280	US-09-508-745-8	Sequence 4, Appli
22	1479	100.0	280	US-09-791-537-46654	Sequence 46654, A
23	1479	100.0	280	US-09-791-537-86366	Sequence 86366, A
24	1479	100.0	280	US-09-155-327B-7	Sequence 7, Appli
25	1479	100.0	280	US-09-508-745-2	Sequence 2, Appli
26	1479	100.0	280	US-09-791-537-75012	Sequence 75012, A
27	1479	100.0	280	US-09-925-674A-7	Sequence 7, Appli
28	1479	100.0	280	US-09-155-327B-7	Sequence 7, Appli
29	1479	100.0	280	US-09-508-745-6	Sequence 6, Appli
30	1479	100.0	280	US-10-221-579-11850	Sequence 11850, A
31	1479	100.0	280	US-09-639-245-2	Sequence 2, Appli
32	1479	100.0	280	PCT-US02-03547-18	Sequence 18, Appli
33	1479	100.0	280	US-10-071-174-18	Sequence 18, Appli
34	1479	100.0	280	PCT-US00-14451-2	Sequence 2, Appli
35	1479	100.0	280	PCT-US99-22448-2	Sequence 2, Appli
36	1479	100.0	280	US-08-160-067-8	Sequence 8, Appli
37	1479	100.0	280	US-08-320-157-14	Sequence 14, Appli
38	1479	100.0	280	US-08-470-865-14	Sequence 14, Appli
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40	1479	100.0	280	US-08-634-995-4	Sequence 4, Appli
41	1479	100.0	280	US-08-915-243-4	Sequence 4, Appli
42	1479	100.0	280	US-09-456-357-48	Sequence 48, Appli
43	1479	100.0	280	US-09-633-200-14	Sequence 14, Appli
44	1479	100.0	280	US-09-734-846-2	Sequence 2, Appli
45	1479	100.0	280	US-09-806-637-2	Sequence 2, Appli

#### ALIGNMENTS

RESULT 1  
; Sequence 3, Application US/07927681  
; GENERAL INFORMATION:  
; APPLICANT: HORVITZ, H. Robert  
; APPLICANT: Hengartner, Michael  
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A  
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02173-4799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/927,681  
; FILING DATE: 10-AUG-1992  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: MIT-5934A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 861-6240  
 TELEFAX: (617) 861-9540  
 TELEX: 951794  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 280 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-07-927-681-3

Query Match 100.0%; Score 1479; DB 3; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-152;  
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 |||||||  
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 Db 61 SIGSIDKINDWEPRLDIEGFVVDYFTHRIKONGMEMFGAPGLPCGVQPEHEMRYMG 120  
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 Db 121 TIFEKKAHNEFTCEOLLAVPRISFSLYQDVVRTVGNAAQDQCPMSYGRLLGLISFGGF 180  
 QY 181 VAAKMESEVLOGVARNLFVYTSLEFKTRIRNNMKEHNRSMDDFTLTKOKMEDYERAE 240  
 |||||||  
 Db 181 VAAKMESEVLOGVARNLFVYTSLEFKTRIRNNMKEHNRSMDDFTLTKOKMEDYERAE 240  
 QY 241 EKVGRKONRRMSMIGAGVTAGATGIVGVVCGRMFSIK 280  
 |||||||  
 Db 241 EKVGRKONRRMSMIGAGVTAGATGIVGVVCGRMFSIK 280

## RESULT 2

US-08-288-295-3  
 ; Sequence 3, Application US/08288295  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Horvitz, H. Robert  
 ; APPLICANT: Hengartner, Michael  
 ; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A  
 ; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED  
 ; TITLE OF INVENTION: CELL DEATH AND USES THEREFOR  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FISH & RICHARDSON  
 ; STREET: 225 Franklin Street, Suite 3100  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: U.S.A. (F) ZIP: 02110-2804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: floppy disk  
 ; OPERATING SYSTEM: IBM PC compatible  
 ; SOFTWARE: PC-DOS/MS-DOS  
 ; SOFTWARE: Wordperfect 5.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/288, 295  
 ; FILING DATE: 10-AUG-1994  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/927,681  
 ; FILING DATE: 10-AUG-1992  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Clark, Paul T.  
 ; REGISTRATION NUMBER: 30,162  
 ; REFERENCE/DOCKET NUMBER: 01997/201003  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 280 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-288-295-3

Query Match 100.0%; Score 1479; DB 6; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-152;  
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKGTPTDFGINSDAQDLPSPSRQASTRRM 60  
 |||||||  
 Db 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKGTPTDFGINSDAQDLPSPSRQASTRRM 60  
 QY 61 SIGSIDKINDWEPRLDIEGFVVDYFTHRIKONGMEMFGAPGLPCGVQPEHEMRYMG 120  
 |||||||  
 Db 61 SIGSIDKINDWEPRLDIEGFVVDYFTHRIKONGMEMFGAPGLPCGVQPEHEMRYMG 120  
 QY 121 TIFEKKAHNEFTCEOLLAVPRISFSLYQDVVRTVGNAAQDQCPMSYGRLLGLISFGGF 180  
 |||||||  
 Db 121 TIFEKKAHNEFTCEOLLAVPRISFSLYQDVVRTVGNAAQDQCPMSYGRLLGLISFGGF 180  
 QY 181 VAAKMESEVLOGVARNLFVYTSLEFKTRIRNNMKEHNRSMDDFTLTKOKMEDYERAE 240  
 |||||||  
 Db 181 VAAKMESEVLOGVARNLFVYTSLEFKTRIRNNMKEHNRSMDDFTLTKOKMEDYERAE 240  
 QY 241 EKVGRKONRRMSMIGAGVTAGATGIVGVVCGRMFSIK 280  
 |||||||  
 Db 241 EKVGRKONRRMSMIGAGVTAGATGIVGVVCGRMFSIK 280

## RESULT 3

US-08-320-157-19  
 ; Sequence 19, Application US/08320157  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIEFER, MICHAEL C.  
 ; APPLICANT: BARR, PHILIP J.  
 ; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
 ; TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF  
 ; NUMBER OF SEQUENCES: 22  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: MORRISON & FOERSTER  
 ; STREET: 755 Page Mill Road  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94304-1018  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: floppy disk  
 ; OPERATING SYSTEM: IBM PC compatible  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/320,157  
 ; FILING DATE: 07-OCT-1994  
 ; CLASSIFICATION: 530  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: LEHNHARDT, SUSAN K.  
 ; REGISTRATION NUMBER: 33,943  
 ; REFERENCE/DOCKET NUMBER: 23647-20007, 20  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 813-5600  
 ; TELEFAX: (415) 494-0792  
 ; TELEX: 706141  
 ; INFORMATION FOR SEQ ID NO: 19:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 280 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single

TOPOLOGY: linear  
US-08-320-157-19

Query Match 100.0%; Score 1479; DB 7; Length 280;  
Best Local Similarity 100.0%; Pred. No. 3.3e-152;  
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRCTADNSLNPAYRRRTMATGEMKEFLIGKTEPTDGINSDADLPSPRQASTRRM 60  
DB 1 MTRCTADNSLNPAYRRRTMATGEMKEFLIGKTEPTDGINSDADLPSPRQASTRRM 60  
QY 61 SIGSISDGKINDMEPRLDIEGFVVDYFTHIRONGMFMFGAPGLPCGVOPHEHMRVYG 120  
DB 61 SIGSISDGKINDMEPRLDIEGFVVDYFTHIRONGMFMFGAPGLPCGVOPHEHMRVYG 120  
QY 121 TIFKKHAENFTFCQDLAVPRISFLYQDVVTVGNADQCPMSYGRILGLISFGF 180  
DB 121 TIFKKHAENFTFCQDLAVPRISFLYQDVVTVGNADQCPMSYGRILGLISFGF 180  
QY 181 VAAKMMESVELQGVRLNLFVYTSLFIKTRIRNNKKEHNSWDPEFTLKGKMEYERAE 240  
DB 181 VAAKMMESVELQGVRLNLFVYTSLFIKTRIRNNKKEHNSWDPEFTLKGKMEYERAE 240  
QY 241 EKVGRRKONRRMSMIGAGVTAGIGVGVVCGRMFSLK 280  
DB 241 EKVGRRKONRRMSMIGAGVTAGIGVGVVCGRMFSLK 280

## RESULT 4

US-08-470-865-19  
Sequence 19, Application US/08470865

GENERAL INFORMATION:  
APPLICANT: KIEFER, MICHAEL C.  
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/470,865  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/320,157  
FILING DATE: 07-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: LEHNHARDT, SUSAN K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 23647-20007.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141

INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 280 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-470-865-19

Query Match 100.0%; Score 1479; DB 8; Length 280;

Best Local Similarity 100.0%; Pred. No. 3.3e-152;  
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRCTADNSLNPAYRRRTMATGEMKEFLIGKTEPTDGINSDADLPSPRQASTRRM 60  
DB 1 MTRCTADNSLNPAYRRRTMATGEMKEFLIGKTEPTDGINSDADLPSPRQASTRRM 60  
QY 61 SIGSISDGKINDMEPRLDIEGFVVDYFTHIRONGMFMFGAPGLPCGVOPHEHMRVYG 120  
DB 61 SIGSISDGKINDMEPRLDIEGFVVDYFTHIRONGMFMFGAPGLPCGVOPHEHMRVYG 120  
QY 121 TIFKKHAENFTFCQDLAVPRISFLYQDVVTVGNADQCPMSYGRILGLISFGF 180  
DB 121 TIFKKHAENFTFCQDLAVPRISFLYQDVVTVGNADQCPMSYGRILGLISFGF 180  
QY 181 VAAKMMESVELQGVRLNLFVYTSLFIKTRIRNNKKEHNSWDPEFTLKGKMEYERAE 240  
DB 181 VAAKMMESVELQGVRLNLFVYTSLFIKTRIRNNKKEHNSWDPEFTLKGKMEYERAE 240  
QY 241 EKVGRRKONRRMSMIGAGVTAGIGVGVVCGRMFSLK 280  
DB 241 EKVGRRKONRRMSMIGAGVTAGIGVGVVCGRMFSLK 280

## RESULT 5

US-08-801-248-3  
Sequence 3, Application US/08801248

GENERAL INFORMATION:  
APPLICANT: Horvitz, H. Robert  
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A  
TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & RICHARDSON  
STREET: 225 Franklin Street, Suite 3100  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/801,248  
FILING DATE: 19-FEB-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/288,295  
FILING DATE: 10-AUG-1994  
APPLICATION NUMBER: US 07/927,681  
FILING DATE: 10-AUG-1992  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 01997/201003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 280 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-801-248-3

Query Match 100.0%; Score 1479; DB 12; Length 280;

Best Local Similarity 100.0%; Pred. No. 3.3e-152;  
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSDAODLPSPSROASTRRM 60  
Db 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSDAODLPSPSROASTRRM 60  
QY 61 SIGESIDKINDMEPRLDIEGFVVDYFTTHIRIRONGMEMFGAPGLPCGVOPHEHMMRVMG 120  
Db 61 SIGESIDKINDMEPRLDIEGFVVDYFTTHIRIRONGMEMFGAPGLPCGVOPHEHMMRVMG 120  
QY 121 TIFEKKAENEFTECEOLLAVPRISFLYODVVRTVGNADTDCCPMSYGRLLIGLSFGGF 180  
Db 121 TIFEKKAENEFTECEOLLAVPRISFLYODVVRTVGNADTDCCPMSYGRLLIGLSFGGF 180  
QY 181 VAAKMESVELOGVRLNLFVYTSLEFKTRIRNNMKEHNSMDPMTLGKMKEDYERAEA 240  
Db 181 VAAKMESVELOGVRLNLFVYTSLEFKTRIRNNMKEHNSMDPMTLGKMKEDYERAEA 240  
QY 241 EKVGRRKQNRMSMIGAGVTAGAGIIVGVVCGRRMFSLK 280  
Db 241 EKVGRRKQNRMSMIGAGVTAGAGIIVGVVCGRRMFSLK 280

## RESULT 6

US-09-633-200-19  
; Sequence 19, Application US/09633200  
; GENERAL INFORMATION:  
; APPLICANT: KIEFER, MICHAEL C.  
; BARR, PHILIP J.  
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA  
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/633,200  
; FILING DATE: 07-Aug-2000  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/320,157  
; FILING DATE: 07-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LEHNHARDT, SUSAN K.  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 23647-20007.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 280 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-09-633-200-19

Query Match 100.0%; Score 1479; DB 20; Length 280;  
Best Local Similarity 100.0%; Pred. No. 3.3e-152;  
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSDAODLPSPSROASTRRM 60  
Db 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSDAODLPSPSROASTRRM 60  
QY 61 SIGESIDKINDMEPRLDIEGFVVDYFTTHIRIRONGMEMFGAPGLPCGVOPHEHMMRVMG 120  
Db 61 SIGESIDKINDMEPRLDIEGFVVDYFTTHIRIRONGMEMFGAPGLPCGVOPHEHMMRVMG 120  
QY 121 TIFEKKAENEFTECEOLLAVPRISFLYODVVRTVGNADTDCCPMSYGRLLIGLSFGGF 180  
Db 121 TIFEKKAENEFTECEOLLAVPRISFLYODVVRTVGNADTDCCPMSYGRLLIGLSFGGF 180  
QY 181 VAAKMESVELOGVRLNLFVYTSLEFKTRIRNNMKEHNSMDPMTLGKMKEDYERAEA 240  
Db 181 VAAKMESVELOGVRLNLFVYTSLEFKTRIRNNMKEHNSMDPMTLGKMKEDYERAEA 240  
QY 241 EKVGRRKQNRMSMIGAGVTAGAGIIVGVVCGRRMFSLK 280  
Db 241 EKVGRRKQNRMSMIGAGVTAGAGIIVGVVCGRRMFSLK 280

## RESULT 7

US-09-791-537-10912  
; Sequence 10912, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Blonomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10912  
; LENGTH: 280  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-09-791-537-10912

Query Match 100.0%; Score 1479; DB 21; Length 280;  
Best Local Similarity 100.0%; Pred. No. 3.3e-152;  
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSDAODLPSPSROASTRRM 60  
Db 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSDAODLPSPSROASTRRM 60  
QY 61 SIGESIDKINDMEPRLDIEGFVVDYFTTHIRIRONGMEMFGAPGLPCGVOPHEHMMRVMG 120  
Db 61 SIGESIDKINDMEPRLDIEGFVVDYFTTHIRIRONGMEMFGAPGLPCGVOPHEHMMRVMG 120  
QY 121 TIFEKKAENEFTECEOLLAVPRISFLYODVVRTVGNADTDCCPMSYGRLLIGLSFGGF 180  
Db 121 TIFEKKAENEFTECEOLLAVPRISFLYODVVRTVGNADTDCCPMSYGRLLIGLSFGGF 180  
QY 181 VAAKMESVELOGVRLNLFVYTSLEFKTRIRNNMKEHNSMDPMTLGKMKEDYERAEA 240  
Db 181 VAAKMESVELOGVRLNLFVYTSLEFKTRIRNNMKEHNSMDPMTLGKMKEDYERAEA 240  
QY 241 EKVGRRKQNRMSMIGAGVTAGAGIIVGVVCGRRMFSLK 280  
Db 241 EKVGRRKQNRMSMIGAGVTAGAGIIVGVVCGRRMFSLK 280

## RESULT 8

US-09-993-420A-3  
; Sequence 3, Application US/09993420A  
; GENERAL INFORMATION:  
; APPLICANT: Horvitz, H. Robert  
; APPLICANT: Hengartner, Michael  
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A

```

; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; FILE OF INVENTION: US0993420A
; FILE REFERENCE: 01997/201006
; CURRENT APPLICATION NUMBER: US/09/993,420A
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 09/234,186
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 07/898,933
; PRIOR FILING DATE: 1992-06-12
; PRIOR APPLICATION NUMBER: 07/927,681
; PRIOR FILING DATE: 1992-08-10
; PRIOR APPLICATION NUMBER: 08/288,295
; PRIOR FILING DATE: 1994-08-10
; PRIOR APPLICATION NUMBER: 08/801,248
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-993-420a-3

```

```

Query Match          100.0%; Score 1479; DB 23; Length 280;
Best Local Similarity 100.0%; Pred. No. 3.3e-152;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADODLPSPROASTRRM 60
   |||||||
DB 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADODLPSPROASTRRM 60
QY 61 SIGESIDKINDMEPRDLIEGFVVDYFTHIRONGMEMFGAPGLPCGVOPHEHMRVWG 120
   |||||||
DB 61 SIGESIDKINDMEPRDLIEGFVVDYFTHIRONGMEMFGAPGLPCGVOPHEHMRVWG 120
QY 121 TFEKKHAENFETFEQOLLAVPRISFSLYODVVRVGNADQDCPMSYGRILGLISFGGF 180
   |||||||
DB 121 TFEKKHAENFETFEQOLLAVPRISFSLYODVVRVGNADQDCPMSYGRILGLISFGGF 180
QY 181 VAAKMMESVELOGVRNLFVYTSLFKTRIRNNKKEHNRSMDDFWTLGKOKMEDYERAE 240
   |||||||
DB 181 VAAKMMESVELOGVRNLFVYTSLFKTRIRNNKKEHNRSMDDFWTLGKOKMEDYERAE 240
QY 241 EKVGRRKRRMSMIGAGVTAGAGIAGVYVCGRMFSLK 280
   |||||||
DB 241 EKVGRRKRRMSMIGAGVTAGAGIAGVYVCGRMFSLK 280

```

```

RESULT 9
; US-10-101-482-19
; Sequence 19, Application US/10101482
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/101,482
; FILING DATE: 18-Mar-2002
; CLASSIFICATION: <Unknown>

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:

```

```

Query Match          100.0%; Score 1479; DB 25; Length 280;
Best Local Similarity 100.0%; Pred. No. 3.3e-152;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADODLPSPROASTRRM 60
   |||||||
DB 1 MTRCTADNSLTNPAYRRRTMATGEMKEFLGKTEPTDFGINSADODLPSPROASTRRM 60
QY 61 SIGESIDKINDMEPRDLIEGFVVDYFTHIRONGMEMFGAPGLPCGVOPHEHMRVWG 120
   |||||||
DB 61 SIGESIDKINDMEPRDLIEGFVVDYFTHIRONGMEMFGAPGLPCGVOPHEHMRVWG 120
QY 121 TFEKKHAENFETFEQOLLAVPRISFSLYODVVRVGNADQDCPMSYGRILGLISFGGF 180
   |||||||
DB 121 TFEKKHAENFETFEQOLLAVPRISFSLYODVVRVGNADQDCPMSYGRILGLISFGGF 180
QY 181 VAAKMMESVELOGVRNLFVYTSLFKTRIRNNKKEHNRSMDDFWTLGKOKMEDYERAE 240
   |||||||
DB 181 VAAKMMESVELOGVRNLFVYTSLFKTRIRNNKKEHNRSMDDFWTLGKOKMEDYERAE 240
QY 241 EKVGRRKRRMSMIGAGVTAGAGIAGVYVCGRMFSLK 280
   |||||||
DB 241 EKVGRRKRRMSMIGAGVTAGAGIAGVYVCGRMFSLK 280

```

```

RESULT 10
; US-09-508-745-8
; Sequence 8, Application US/09508745
; GENERAL INFORMATION:
; APPLICANT: Cory, Suzanne
; APPLICANT: Adams, Jerry
; APPLICANT: Print, Chris
; APPLICANT: Gibson, Leonie
; TITLE OF INVENTION: A METHOD OF TREATMENT AND AN ANIMAL MODEL USEFUL FOR
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 13464
; CURRENT APPLICATION NUMBER: US/09/508,745
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: PCT/A098/00764
; PRIOR FILING DATE: 1998-09-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-508-745-8

```

```

Query Match          11.2%; Score 166; DB 19; Length 193;
Best Local Similarity 26.1%; Pred. No. 6.6e-09;
Matches 55; Conservative 28; Mismatches 90; Indels 38; Gaps 8;

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01  Y  DIEGCVVDYFTHRIQNGEMEWGAGLPGCVQPEHEMMHVMGTIFPKKHAENDETCEOL 138
02  Db 9 DTRALVADEYVGRIRLQKQYVCAGGEGEPAADPLHQAMAAAGDEFTTRRRRTFSDLAOL 68
03  QY 139 IAVP-----RISFSYXQDVYRTVGNAQTDQCPMSYGRLLIGLISFGGEVAKMM--ES 188
04  Db 69 HVTPSAQQRFTQVSDDELFGQ-----GPNMGRILVAFVFGAALCAESYVKEM 115
05  QY 189 VELQGVQRRLFYTTSLFIKTRIRNNMKHNRSWDQFMTL-GQMKEDYRRALEKYGRRK 247
06  Db 116 EPLVQGVQDWIV---AYLETRILA-PMIHSSGGWADFTALYIGDALED-----ARRL 162
07  QY 248 QNRKRSMIGAGVTAGACIGVGVVCCGRMFS 278
08  Db 163 REGNMASVSTVYT-GAVALGALVTYGAFFAS 192
09  RESULT 11
10  US-09-155-327B-9
11  ; Sequence 9, Application US/09155327B
12  ; GENERAL INFORMATION:
13  ; APPLICANT: AMRAD Operations Pty Ltd
14  ; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2
15  ; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
16  ; FILE REFERENCE: 2096584
17  ; CURRENT APPLICATION NUMBER: US/09/155,327B
18  ; CURRENT FILING DATE: 1999-03-29
19  ; PRIOR APPLICATION NUMBER: PM8965
20  ; PRIOR FILING DATE: 1996-03-27
21  ; NUMBER OF SEQ ID NOS: 9
22  ; SOFTWARE: PatentIn Ver. 2.1
23  ; SEQ ID NO 9
24  ; LENGTH: 192
25  ; TYPE: PRT
26  ; ORGANISM: Mouse
27  US-09-155-327B-9

```

```

Query Match      10.9%; Score 161.5; DB 15; Length 192;
Best Local Similarity 25.6%; Pred. No. 2e-08;
Matches 54; Conservative 29; Mismatches 89; Indels 39; Gaps 8

QY      79 DIEGVVDVYFTTRIRIQNGMEWFGAPGLPCGVOPENHEMHKMGCTIEFKHAENETFCQOL 138
      | | | : : | | | | | | | | | | | | | | | | | | | | | | | |
DB      9 DTRALVADPVGVRRLQKGVCGAGGEGPAAADPLHQAMRAADGDEFETRRRRFSDLAAL 68

QY      139 IAVP-----RISLSLYQDVYRVYVGNACTOCPMSYGRLLIGLSFSGFVAKKM--ES 188
      | | | : : | | | | | | | | | | | | | | | | | | | | | | | |
DB      69 HVTPESSAQQRTFOVSDLELFG-----GPNMRRLVAFFVFGALCAESYVKEM 115

QY      189 VELQGOVRLRFYTSLEFTRIRIRINMKHENRSMWDEPMTL-GKQMKDREAEAEKVGRRK 247
      | | | | : : : : : : : : : : : : | | | | | | | | | | | |
DB      116 EPLVQOVQDWIV---AYLETRLA-DWIRHSGGKADFTALYIGGALD-----ARKL 162

QY      248 QNRKSMIGAGVTAGAIGIVGVVCGRRMFS 278
      | | : : : | | | : : | | | | |
DB      163 REGNNAV--STVVTGAVLALGALVTVGAFPAS 191

RESULT 12
PCT-US97-15872--84
; Sequence 84, Application PC/TUS9715872
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63146

; COMPUTER READABLE FORM:
;

```

```

1      MEDIUM TYPE: Floppy disk
2
3      COMPUTER: IBM PC compatible
4
5      OPERATING SYSTEM: PC-DOS/MS-DOS
6
7      SOFTWARE: PatentIn Release #1.0, Version #1.30
8
9      CURRENT APPLICATION DATA:
10     APPLICATION NUMBER: PCT/US97/15872
11
12     FILING DATE:
13
14     CLASSIFICATION:
15
16     PRIOR APPLICATION DATA:
17     APPLICATION NUMBER: US 08/706,741
18     FILING DATE: 09-SEP-1996
19
20     ATTORNEY/AGENT INFORMATION:
21
22     NAME: HOLLAND, DONALD R.
23     REGISTRATION NUMBER: 35,197
24     REFERENCE/DOCKET NUMBER: 965017
25
26     TELECOMMUNICATION INFORMATION:
27
28     TELEPHONE: (314) 727-5188
29     TELEFAX: (314) 727-6092
30
31     INFORMATION FOR SEQ ID NO: 84:
32     SEQUENCE CHARACTERISTICS:
33     LENGTH: 27 amino acids
34     TYPE: amino acid
35     STRANDEDNESS:
36     TOPOLOGY: linear
37
38     MOLECULE TYPE: peptide
39
40     PCT-US97-15872-84

```

```

Query Match          10.5%; Score 156; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4,1e-09;
Matches    27; Conservative    0; Mismatches    0; Indels    0; Gaps    0

QY      73 WEPRLDIEGFVVDYETHRRIRONGNEW 99
        |||
Db       1 WEPRLDIEGFVVDYETHRRIRONGNEW 27

RESULT 13
US-08-706-741-84
: Sequence 84, Application US/08706741
: GENERAL INFORMATION:
: APPLICANT: KORSMEYER, STANLEY J.
: TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: HOWELL & HAFERKAMP, L.C.
: STREET: 7733 FORSYTH BLVD., SUITE 1400
: CITY: ST. LOUIS
: STATE: MISSOURI
: COUNTRY: USA
: ZIP: 63146
: COMPUTER READABLE FORM:
: MEDIUM TYPE: FLOPPY disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/706,741
: FILING DATE:
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: HOLLAND, DONALD R.
: REGISTRATION NUMBER: 35,197
: REFERENCE/DOCKET NUMBER: 965017
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (314) 727-5188
: TELEFAX: (314) 727-6092
: INFORMATION FOR SEQ ID NO: 84:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 27 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide

```



US-08-706-741-84

Query Match 10.5%; Score 156; DB 11; Length 27;

Best Local Similarity 100.0%; Pred. No. 4.1e-09;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 WEPRLDIEGFVVDYFTHIRONGMEW 99

DB 1 WEPRLDIEGFVVDYFTHIRONGMEW 27

RESULT 14

US-08-706-741A-84

Sequence 84, Application US/08706741A

GENERAL INFORMATION:

APPLICANT: KORSMEYER, STANLEY J.

TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOWELL &amp; HAERKAMP, L.C.

STREET: 7733 FORSYTH BLVD., SUITE 1400

CITY: ST. LOUIS

STATE: MISSOURI

COUNTRY: USA

ZIP: 63146

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/706,741A

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, DONALD R.

REGISTRATION NUMBER: 35,197

REFERENCE/DOCKET NUMBER: 965017

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 727-5188

TELEFAX: (314) 727-6092

INFORMATION FOR SEQ. ID NO: 84:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-706-741A-84

Query Match 10.5%; Score 156; DB 11; Length 27;

Best Local Similarity 100.0%; Pred. No. 4.1e-09;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 WEPRLDIEGFVVDYFTHIRONGMEW 99

DB 1 WEPRLDIEGFVVDYFTHIRONGMEW 27

RESULT 15

US-08-733-505-49

Sequence 49, Application US/08733505

GENERAL INFORMATION:

APPLICANT: KORSMEYER, STANLEY J.

TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOWELL &amp; HAERKAMP, L.C.

STREET: 7733 FORSYTH BLVD., SUITE 1400

CITY: ST. LOUIS

STATE: MISSOURI

COUNTRY: USA

ZIP: 63105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/733,505

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, DONALD R.

REGISTRATION NUMBER: 35,197

REFERENCE/DOCKET NUMBER: 965458

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 727-5188

TELEFAX: (314) 727-6092

INFORMATION FOR SEQ. ID NO: 49:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-733-505-49

Query Match 10.5%; Score 156; DB 11; Length 27;

Best Local Similarity 100.0%; Pred. No. 4.1e-09;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 WEPRLDIEGFVVDYFTHIRONGMEW 99

DB 1 WEPRLDIEGFVVDYFTHIRONGMEW 27

Search completed: February 24, 2003, 11:57:57

Job time : 146 secs

•  
•  
•  
•



[illegible]





Db 9 VVDFLSYKLSQKGYWSQFSVDEENRTAEPEERETPSAINGNPSWHLADSPAVNGA 68  
QY 115 -----MMRVMTGTFEKKHAENFETCEOLLAVPRISFSLYODVVR 154  
Db 69 TGHSSSLDAREVYIPMAAVKQALREAGDEFELRYRRAFSDLTSLHTTGTAYOSFEOVYN 128  
QY 155 TVGNAQTDQCPMSYGRLLIGLISFGGFVAAKMMESV--ELQGOVRLFYVTSLEFKTRIRN 212  
Db 129 -----ELFRDGVNMGRIYVAFSPFGG---ALCVESYDKEMQVLSRIAAMATYLDHLE 179  
QY 213 NMKEHNSWDPEMTLGKQMKEDY-ERAEAEKVGRRKQNRKMSMIGAGVTAGATIGVGVV 271  
Db 180 PWIOENGMDTFEVL-----YGNNAAESRKGOERFNFWLTG-----MTVAGVVL 225  
QY 272 CGRMFSLK 280  
Db 226 LG-SLFSRK 233

RESULT 13  
US-10-302-262-2  
; Sequence 2, Application US/10302262  
; GENERAL INFORMATION:  
; APPLICANT: Benmett, C. Frank  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Nickoloff, Brian J.  
; APPLICANT: Zhang, Qionglou  
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
; FILE REFERENCE: ISPh-0528  
; CURRENT APPLICATION NUMBER: US/10/302,262  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US/09/734,846  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 09/277,020  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 09/167,921  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 09/323,743  
; PRIOR FILING DATE: 1999-06-02  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-302-262-2

Query Match 9.1%; Score 135; DB 6; Length 233;  
Best Local Similarity 21.3%; Pred. No. 9.4e-06;  
Matches 53; Conservative 38; Mismatches 82; Indels 76; Gaps 10;

QY 84 VVDYFTHRIKONGMEWF-----GAPGLPCGVOPRHE----- 114  
Db 9 VVDFLSYKLSQKGYWSQFSVDEENRTAEPEERETPSAINGNPSWHLADSPAVNGA 68  
QY 115 -----MMRVMTGTFEKKHAENFETCEOLLAVPRISFSLYODVVR 154  
Db 69 TGHSSSLDAREVYIPMAAVKQALREAGDEFELRYRRAFSDLTSLHTTGTAYOSFEOVYN 128  
QY 155 TVGNAQTDQCPMSYGRLLIGLISFGGFVAAKMMESV--ELQGOVRLFYVTSLEFKTRIRN 212  
Db 129 -----ELFRDGVNMGRIYVAFSPFGG---ALCVESYDKEMQVLSRIAAMATYLDHLE 179  
QY 213 NMKEHNSWDPEMTLGKQMKEDY-ERAEAEKVGRRKQNRKMSMIGAGVTAGATIGVGVV 271  
Db 180 PWIOENGMDTFEVL-----YGNNAAESRKGOERFNFWLTG-----MTVAGVVL 225  
QY 272 CGRMFSLK 280  
Db 226 LG-SLFSRK 233

RESULT 14  
US-10-169-223-10  
; Sequence 10, Application US/10169223  
; GENERAL INFORMATION:  
; APPLICANT: Shimizu, Shigeomi  
; APPLICANT: TSUTIMOTO, Yoshihide  
; TITLE OF INVENTION: BH4-Fused Polypeptides  
; FILE REFERENCE: 1422-0537P  
; CURRENT APPLICATION NUMBER: US/10/169,223  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: JP 11-371449  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: PCT/JP00/09274  
; PRIOR FILING DATE: 2000-12-26  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-169-223-10

Query Match 9.1%; Score 135; DB 6; Length 233;  
Best Local Similarity 21.3%; Pred. No. 9.4e-06;  
Matches 53; Conservative 38; Mismatches 82; Indels 76; Gaps 10;

QY 84 VVDYFTHRIKONGMEWF-----GAPGLPCGVOPRHE----- 114  
Db 9 VVDFLSYKLSQKGYWSQFSVDEENRTAEPEERETPSAINGNPSWHLADSPAVNGA 68  
QY 115 -----MMRVMTGTFEKKHAENFETCEOLLAVPRISFSLYODVVR 154  
Db 69 TGHSSSLDAREVYIPMAAVKQALREAGDEFELRYRRAFSDLTSLHTTGTAYOSFEOVYN 128  
QY 155 TVGNAQTDQCPMSYGRLLIGLISFGGFVAAKMMESV--ELQGOVRLFYVTSLEFKTRIRN 212  
Db 129 -----ELFRDGVNMGRIYVAFSPFGG---ALCVESYDKEMQVLSRIAAMATYLDHLE 179  
QY 213 NMKEHNSWDPEMTLGKQMKEDY-ERAEAEKVGRRKQNRKMSMIGAGVTAGATIGVGVV 271  
Db 180 PWIOENGMDTFEVL-----YGNNAAESRKGOERFNFWLTG-----MTVAGVVL 225  
QY 272 CGRMFSLK 280  
Db 226 LG-SLFSRK 233

RESULT 15  
US-10-169-223-14  
; Sequence 14, Application US/10169223  
; GENERAL INFORMATION:  
; APPLICANT: Shimizu, Shigeomi  
; APPLICANT: TSUTIMOTO, Yoshihide  
; TITLE OF INVENTION: BH4-Fused Polypeptides  
; FILE REFERENCE: 1422-0537P  
; CURRENT APPLICATION NUMBER: US/10/169,223  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: JP 11-371449  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: PCT/JP00/09274  
; PRIOR FILING DATE: 2000-12-26  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 212  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: CDS of Synthesized DNA for mutant bcl-xL  
US-10-169-223-14

Query Match 8.6%; Score 126.5; DB 6; Length 212;  
Best Local Similarity 25.3%; Pred. No. 6.1e-05;

	Matches	43;	Conservative	33;	Mismatches	67;	Indels	27;	Gaps	8;
QY	114	EMRRVNGTIF	EKKHAENETFC	EQLLAVPRIS	SLYQDVYRTV	GNACTDQCP	MSYGR	LI	173	
DB	67	QALREAGDE	FEELRYRRA	FSDLTSQ	LHITPGTAY	QSEQVYN	----	ELFRDGVN	WGRIVA	121
QY	174	LTSFGGEV	AAKMMESV	-	ELQGOVRNL	FVYTSLE	IKTRIRNN	MKEHNR	SRWDD	FMTLGKOM 231
DB	122	FPSFGG	---	ALCVESYD	KEMQVLS	RIAMMATY	LNDHL	-	EPWIQENG	SGMDTEVEL----- 173
QY	232	KEDY	-	ERAFAEKY	GRKRNRR	MSMIGAGV	TAGAIGIV	VVVCGRM	MSL	280
DB	174	---	YGNNAAES	RKQGR	ENRWF	LTG-----	MTVAGV	VLLG	-	SLFSRK 212

Search completed: February 24, 2003, 11:59:02  
 Job time : 59 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 24, 2003, 11:52:39 ; Search time 18 Seconds  
(without alignments)  
1495.424 Million cell updates/sec

Title: US-09-993-420a-3

Perfect score: 1479  
Sequence: 1 MTRCTADNSLTNPAYRRRRM.....AGATGIVGVVCGMMFSLK 280

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1479	100.0	280	2 AS3189	apoptosis suppressor protein ced-9 (imp
2	1377	93.1	261	2 H88578	apoptosis regulato
3	135	9.1	233	2 B47537	BCL-X protein - ra
4	135	9.1	233	2 S51761	bcl-x long - mouse
5	132	8.9	233	2 I49056	BCL-X-long - rat
6	126	8.5	233	2 I67431	transforming prote
7	116	7.8	233	2 A37332	transforming prote
8	116	7.8	239	1 TVH041	transforming prote
9	113.5	7.7	236	1 TVWSA1	transforming prote
10	113.5	7.7	236	1 I67432	BCL-2 - rat (fragm
11	112	7.6	177	2 S54778	NR-13 protein - qu
12	110.5	7.5	236	2 JC7383	B-cell lymphoma 2
13	109.5	7.4	236	2 I53744	gene bcl-2 protein
14	108	7.3	214	2 I49057	bcl-x transmembran
15	108	7.3	1329	2 AE1901	WD-repeat containi
16	106.5	7.2	232	2 S24390	transforming prote
17	99	6.7	227	2 JE0203	apoptosis regulato
18	96.5	6.5	757	2 F83516	transforming prote
19	95	6.4	199	1 TVWSB1	transforming prote
20	95	6.4	350	2 A47476	BCL2 homolog MCL1
21	94.5	6.4	216	2 B37332	transforming prote
22	90.5	6.1	205	1 TVH0B1	transforming prote
23	90.5	6.1	279	2 H90992	hypothetical prote
24	90.5	6.1	607	2 AH2891	thiamin biosynthes
25	90.5	6.1	644	2 D97667	thiamin biosynthes
26	90	6.1	274	2 A64978	hypothetical prote
27	89.5	6.0	1217	2 F69823	probable phosphoe
28	89	6.0	190	2 A47537	apoptosis regulato
29	88.5	6.0	283	2 C85838	hypothetical prote

30	88	5.9	255	2 JC7567	MCL-1a protein - 2
31	88	5.9	436	2 S13583	nosd protein precu
32	87	5.9	347	2 S35229	hypd' protein - Br
33	86	5.8	384	2 D66821	hydroxymethylgluta
34	85	5.7	1737	2 A57491	hypothetical helic
35	84.5	5.7	150	2 D81356	methyated-DNA-lpr
36	84.5	5.7	430	2 H83178	conserved hypotet
37	84	5.7	383	2 H98287	hypothetical prote
38	83.5	5.6	1657	2 T15838	hypothetical prote
39	83	5.6	361	2 A65050	membrane-bound lyl
40	83	5.6	316	1 XBPVVS	3-phosphoshikimate
41	83	5.6	545	2 B89823	hypothetical prote
42	83	5.6	1112	2 H95964	probable outer mem
43	82.5	5.6	447	2 JC5352	2-nitrofluorene dio
44	82.5	5.6	574	2 T16230	hypothetical prote
45	82.5	5.6	608	2 T51217	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

A:53189  
apoptosis suppressor CED-9 - Caenorhabditis elegans  
N:Alternate names: hypothetical protein T07C4.8; proto-oncogene bcl-2 homolog  
C:Species: Caenorhabditis elegans  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jul-2000  
C:Accession: A53189; S41021  
R:Hengartner, M.O.; Horvitz, H.R.  
Cell 76, 665-676, 1994  
A:Title: Caenorhabditis elegans cell survival gene ced-9 encodes a functional homolog  
A:Reference number: A53189; MUID:94170367; PMID:7907274  
A:Accession: A53189  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-280 <HEN>  
A:Cross-references: GB:L26545; NID:g433174; PIDN:AAA20080.1; PID:g433176  
R:Berts, M.  
submitted to the EMBL Data Library, January 1994  
A:Reference number: S41014  
A:Accession: S41021  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 20-280 <BER>  
A:Cross-references: EMBL:Z29443; NID:g1067051; PID:g443835  
C:Genetics:  
A:Gene: ced-9  
A:Introns: 84/3; 171/3; 22/3

Query Match	Score	1479;	DB 2;	Length	280;
Best Local Similarity	100.0%;	Pred. No. 2.6e-129;			
Matches	280;	Conservative	0;	Mismatches	0;
Indels	0;			Gaps	0;
QY	1	MTRCTADNSLTNPAYRRRRMATGEMKEFLGKGPEDFGINSADQLPSPSROASTRRM	60		
DB	1	MTRCTADNSLTNPAYRRRRMATGEMKEFLGKGPEDFGINSADQLPSPSROASTRRM	60		
QY	61	STGESIDCKINDMEPRLDIEGFVVDYFTFHRIRONGEMFGAPGLPCGVOPPEHMMRVMG	120		
DB	61	STGESIDCKINDMEPRLDIEGFVVDYFTFHRIRONGEMFGAPGLPCGVOPPEHMMRVMG	120		
QY	121	TIFEKKAHNEFTCEOLLAVPRISFYODVFTVGNADTDCPMYGRIGLISGFG	180		
DB	121	TIFEKKAHNEFTCEOLLAVPRISFYODVFTVGNADTDCPMYGRIGLISGFG	180		
QY	181	VAAKMESVEIQGVNLFVYTSLEIKTRIRNNMKEHNRSDDEMTLGKMKEDYEAAEA	240		
DB	181	VAAKMESVEIQGVNLFVYTSLEIKTRIRNNMKEHNRSDDEMTLGKMKEDYEAAEA	240		
QY	241	EKVGRRKONRRSMIGAGVTAGATGIVGVVCGMMFSLK	280		
DB	241	EKVGRRKONRRSMIGAGVTAGATGIVGVVCGMMFSLK	280		

```

RESULT 2
H88578
protein ced-9 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence=revision 10-May-2001 #text_change 10-May-2001
C:Accession: H88578
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: H88578
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1*261 <STO>
A:Cross-references: GB:chr_III; PIDN:CAAB257.1; PID:g3879511; GSPDB:GN00021
C:Genetics:
A:Gene: ced-9
A:Map position: 3

```

Query Match	93.1%	Score 1377;	DB 2;	Length 261;
Best Local Similarity	100.0%	Pred. No. 6.7e-120;		
Matches 261;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	20	MATEKMEFGLIGTETPTDGLINSNAODLPSPSROASTRRMSIGESIDGKINDMEERLD	79
Db	1	MATEKMEFGLIGTETPTDGLINSBODLPSPSROASTRRMSIGESIDGKINDMEERLD	60
QY	80	IEGEVVDYFTHIRONGMEMFGAPGLPCGVOPENHMMVMQITIEKKHAENFETFCOLL	139
Db	61	IEGEVVDYFTHIRONGMEMFGAPGLPCGVOPENHMMVMQITIEKKHAENFETFCOLL	120
QY	140	AVPRISPSLYODPVYRVGNAOTDQCPMSYGRGLIGLISGCGVAAKKMESEVLOGOVNLF	199
Db	121	AVPRISPSLYODPVYRVGNAOTDQCPMSYGRGLIGLISGCGVAAKKMESEVLOGOVNLF	180
QY	200	VYTSLEFKTIRIRNNKMEHNSMDPMTLGKQMKEDYEPAEAKEYGRKORRRMSMIGAGY	259
Db	181	VYTSLEFKTIRIRNNKMEHNSMDPMTLGKQMKEDYEPAEAKEYGRKORRRMSMIGAGY	240
QY	260	TAGAIGIVGVVCGRRMFSLK	280
Db	241	TAGAIGIVGVVCGRRMFSLK	261

RESULT 3  
B47537  
apoptosis regulator bcl-xl - human  
N:Alternate names: bcl-2-related protein  
N:Contains: apoptosis regulator bcl-xs  
C:Species: Homo sapiens (man)  
C:Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 16-Jul-1999  
C:Accession: B47537; C47537  
R:Boise, L.H.; Gonzalez-garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;  
Cell 74, 597-608, 1993  
A>Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptosis  
A:Reference number: A47537; MUID:93364977; PMID:8358789  
A:Accession: B47537  
A:Status: nucleic acid sequence not shown; translated from GR/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-233 <BO>  
A:Cross-references: GB:L20121; NID:g510900; PIDN:CAA80661.1; PID:g510901  
A:Accession: C47537  
A:Status: nucleic acid sequence not shown; translated from GR/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-69, 'G', 71-125, 189-233 <BO>  
A:Cross-references: GB:L20122; NID:g623236; PIDN:CAA80662.1; PID:g623237  
C:Genetics:  
A:Gene: GDB:BC12L  
A:Cross-references: GDB:228079  
C:Superfamily: bcl transforming protein

```

Query Match          9.1%; Score 135; DB 2; Length 233;
Best Local Similarity 21.3%; Pred. No. 7.3e-05;
Matches 33; Conservative 38; Mismatches 82; Indels 76; Gaps 10;
C:Keywords: alternative splicing; apoptosis
F:1.233/P:Product: apoptosis regulator bcl-xL #status predicted <MA>
F:1.125,189-223/P:Product: apoptosis regulator bcl-xs #status predicted <MA>

```

QY	84	VVDFYFHHRIKROGMEMF-----GAGDLGCGVQPEHE-----	114
		: : :	
Db	9	VVDFLKYKLSQGYSGMSQSFSDVEENRRIHAEDEGHESEMETPSALINGNPSPMHLADSEAVNCA	68
QY	115	-----MMRWGTFIEKKHAENFETFCQLLAVPRISESLYQDVR	154
		: : : : :	
Db	69	TAHSSLDAREYIPMAAVKQALREAGDEFLRYRRAFSDLTSQLHTPGTAVOSPEQVY	128
QY	155	TVGNAGTDDCPMSYGRLLGLISFGEPFAAMMMSY--ELIQGVRLNFYITSLFKTRTN	212
		: : : : :	
Db	129	ELFSDGYNMGRIYAFESFG--ALCVSYISREKQIVLVSRIAMKMYINDH-E	179
		: : : : :	
QY	213	NKKEHNRSDDEFTLIGQMKEDY-EERAERVGRRRQNRMSMIGAGYTAGAIGIVVY	271
		: : : : :	
Db	180	PMIOENGCGWDFVEL-----YGNMAAESRSGQGRFRNRLTG-----MIVAGVYL	225
QY	272	CGRMPSLK 280	
		: : :	
Db	226	LG-SLFSTRK 233	

## RESULT 4

S51761

BCL-X protein - rat  
C:Species: Rattus norvegicus (Norway rat)

```
C:\Accession: S51761; S51762
C:\date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 02-Mar-2001
```

submitted to the EMBL Data Library, November 1994  
A:Reference number: S51761

A;Accession: S51761  
A;Status: preliminary

A; Molecule type: DNA  
A; Residues: 1-233 <MTC>

A; Cross-references: EMBL:X82337; NID:g607176; PIDN:CAA57886.1; PID:g607177  
A; Experimental source: embryonic; brain

A/Accession: S51/62  
A/Status: preliminary  
A/Molecular function: none

A; Residues: 1-125, 189-233 <MT2>  
n, molecule type: DNA  
Cross-references: EMBL: Y82537, NID: d6607726, PDB: 1A5E7097 1, PDB: 6607726

A;Note: smaller form due to splicing  
A;Experimental source: embryonic; brain  
FIDN:000/11/0 FIDN:000/80/.1 FID:900/1/0

C;Genetics:  
A;Introns: 125/3

C;Superfamily: bcl transforming protein

Query Match	9.1%;	Score 135;	DB 2;	Length 233
Best local similarity	0.126			
Best local alignment	31.2%			

best local similarity 41.35; Pred. NO. 1-se-05;  
Matches 53; Conservative 38; Mismatches 82; Indels 76; Gaps 10;

OY 84 VVDYFTTHIRIONGMWF-----GAPGLPCGVQPEHE----- 114  
|||::: | | : || |  
Db 9 VVDFLSKLSQSGCYSWSPQSDVEENPTAEPEETPEEPTPSAINGNPSWHLADSPAIVNGA 68

```

OY -----MMRVGTIFEKKAENFETCEQLLAVPRISFSLYQDVVR 154
115 -----
      : | | : | | : | |
69 TGHSSLDAREVIMAAVKCALPACDDEEFLDYBAACEDTECUTLMDMAVACCTHQA 120

```

155 TVGNQTDPCNSYGRLLIGLISGGFVAAKMSV--ELQGVNRLLFVYTSLFKTRIRN 212

Db 129 ----ELFRDGVNMGRIAAFEESFG--ALCVESVDKEMQVLVSRIASMMATYLNDHL-E 179

QY 213 NKEHNRSWDEMTLGKQMKEDY-ERAEAEKVGRRKQNRMSMGIGAVYTAGALIGVYV 271

Db 180 PWIOENGWDTFVDL-----YGNNAASRKQGERFRNMFLLTG-----MTVAGVVL 225

Qy 272 CGRMFSLK 280

Db 226 LG-SLFSRK 233

# RESULT 5

bcl-x long - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999

C:Accession: I49056; S52866

R:Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.

J. Immunol. 153, 4388-4398, 1994

A:Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.

A:Reference number: I49055; MUID:95052604; PMID:7963517

A:Accession: I49056

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-233 <RES>

A:Cross-references: EMBL:U0101; NID:9506647; PIDN:AAA82173.1; PID:9506648

R:Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.

submitted to the EMBL Data Library, November 1994

A:Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line throu

A:Reference number: S52866

A:Accession: S52866

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-233 <KAM>

A:Cross-references: EMBL:X83574; NID:9695622; PIDN:CAA58557.1; PID:9695623

C:Superfamily: bcl transforming protein

## Query Match

Best Local Similarity 20.9%; Score 132; DB 2; Length 233;

Matches 52; Conservative 39; Mismatches 82; Indels 76; Gaps 10;

Qy 84 VVDYFTHIRIRONGMEWF-----GA 102

Db 9 VVDFLSYKLSQKGYSMQSDVEENKTEAPEETEERETPSAINGNPSMHLADSPAVNGA 68

Qy 103 PGLPCGVOPH-----EMRWVGITFEKKAENFETCEQLLAVPRIISLYODVVR 154

Db 69 TGHSSSLDAREVLPMAAVKQALREAGDEFELRYRAFSDLTSQLHTPTGTAVQSEFQVYN 128

Qy 155 TVGNAQTDQCPMSYGRLLIGLISFGGFVAAKMESV--ELQGVNRLFYVTSIFIKTRIRN 212

Db 129 -----ELFRDGVNMGRIYAFESFGG---ALCVESYDKEMQVLVSRIASMAATYLDHL-E 179

Qy 213 NKEHNRSMDDEFTLTKQKMEDEY-ERAFAEKYGRKONRRMSMGAGVTAGATGIVGVV 271

Db 180 PWIOENGWDTFVDL-----YGNNAASRKQGERFRNMFLLTG-----MTVAGVVL 225

Qy 272 CGRMFSLK 280

Db 226 LG-SLFSRK 233

# RESULT 6

bcl-x long - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 16-Jul-1999

C:Accession: I67431

R:Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.

Endocrinology 136, 232-241, 1995

A:Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equi

constitutive bcl-2 and bcl-x long messenger ribonucleic acid levels.

A:Reference number: I53295; MUID:95129487; PMID:7828536

A:Accession: I67431

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-233 <RES>

A:Cross-references: EMBL:U34963; NID:q1004376; PIDN:AAA7686.1; PID:q1004377

C:Superfamily: bcl transforming protein

Query Match 8.5%; Score 126; DB 2; Length 233;

Best Local Similarity 21.6%; Pred. No. 0.0005; Mismatches 54; Conservative 36; Indels 78; Gaps 11;

Qy 84 VVDYFTHIRIRONGMEWF-----GAPGLPCGVOPH----- 114

Db 9 VVDFLSYKLSQKGYSMQSDVEENKTEAPEETEERETPSAINGNPSMHLADSPAVNGA 68

Qy 115 -----MMRWVGITFEKKAENFETCEQLLAVPRIISLYODVVR 154

Db 69 TGHSSSLDAREVLPMAAVKQALREAGDEFELRYRAFSDLTSQLHTPTGTAVQSEFQVYN 128

Qy 155 TVGNAQTDQCPMSYGRLLIGLISFGGFVAAKMESV--ELQGVNRLFYVTSIFIKTRIRN 212

Db 129 -----ELFRDGVNMGRIYAFESFGG---ALCVESYDKEMQVLVSRIASMAATYLDHL-E 179

Qy 213 NKEHNRSMDDEFTLTKQKMEDEY-ERAFAEKYGRKONR--RMSMGAGVTAGATGIVGVV 270

Db 180 PWIOENGWDTFVDL-----YGNNAASRKQGERFRNMFLLTG-----MTVAGVVL 224

Qy 271 CGRMFSLK 280

Db 225 LG-SLFSRK 233

# RESULT 7

A37332 transforming protein (bcl-2-alpha) - chicken

C:Species: Gallus gallus (chicken)

C>Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 23-Feb-1997

C:Accession: A37332; S35453

R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a va

A:Reference number: A37332; MUID:92375724; PMID:1508712

A:Accession: A37332

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-233 <EGU>

A:Cross-references: EMBL:D11381

C:Genetics:

A:Introns: 189/3

C:Superfamily: bcl transforming protein

C:Keywords: mitochondrion; transforming protein; transmembrane protein

Query Match 7.8%; Score 116; DB 2; Length 233;

Best Local Similarity 19.9%; Pred. No. 0.0042;

Matches 48; Conservative 38; Mismatches 77; Indels 78; Gaps 11;

Qy 79 DIEGFVVDYFTHIRIRONGMEWF-----APGLPC----- 107

Db 10 DNREIVLKYTHYKLSQKGYSDVMAAGEDRPVPAAPAAVAAGASHHRRPEPGSA 69

Qy 108 -----GVOPH-----HEMRVVGITFEKKAENFETCEQLLAVPRIISLYODVVR 154

Db 70 AASEVPAEGLRPAAPGVHIALRQAGDEFRRORDPAQMSGDLHLTP---FTAHGFEVA 126

Qy 155 TVGNAQTDQCPMSYGRLLIGLISFGGFVAAKMESV--ELQGVNRLFYVTSIFIKTRIRN 212

Db 127 VVEELFRD--GVNMGRIYAFESFGVAC---VESVNRKMSPLDNTATMTETLNRHL-H 180

Qy 213 NKEHNRSMDDEFTLTKQKMEDEY-ERAFAEKYGRKONRRM-----SMIGAGVTAG 262

Db 181 NWIDNGWDFAVELYSGMSKPLPDES-----WISLKITLSLVIVGACITITG 227

Qy 263 A 263

Db 228 A 228

## RESULT 8

TVHDA1

transforming protein bcl-2, splice form alpha - human

C:Species: Homo sapiens (man)

C&gt;Date: 31-Dec-1988 #sequence\_revision 07-Jun-1996 #text\_change 15-Oct-1999

C:Accession: G37332; A29409; S02452; A24428; A27622; B27622

R:Enguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety

A:Reference number: A37332; MUID:92375724; PMID:1508712

A:Accession: C37332

A:Status: nucleic acid sequence not shown: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-239 &lt;EGU&gt;

A:Note: this report is a correction

R:Tsujimoto, Y.; Croce, C.M.

Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986

A:Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene

A:Reference number: A29409; MUID:86259760; PMID:3523487

A:Accession: A29409

A:Molecule type: mRNA

A:Residues: 1-95, 'A', 'G', '111-236, 'S', '238-239 &lt;TSD&gt;

A:Cross-references: GB:M13994; NID:q179366; PIDN:AAA51813.1; PID:q179367

A:Note: this sequence has been corrected in reference A37332

R:Seio, W.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, P.; Korsmeyer

EMBO J. 7, 123-131, 1988

A:Title: Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2

A:Reference number: S02452; MUID:88196071; PMID:2834197

A:Accession: S02452

A:Molecule type: mRNA

A:Residues: 1-239 &lt;SET&gt;

R:Cleary, M.L.; Smith, S.D.; Sklar, J.

Cell 47, 19-28, 1986

A:Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin

A:Reference number: A24428; MUID:87002488; PMID:2875799

A:Accession: A24428

A:Molecule type: mRNA

A:Residues: 1-58, 'T', '60-116, 'R', '118-239 &lt;CLE&gt;

A:Cross-references: GB:M14745; NID:q179370; PIDN:AAA5591.1; PID:q179371

R:Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakshi, A.

Oncogene Res. 2, 263-275, 1988

A:Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma:

A:Reference number: A27622; MUID:88217344; PMID:3285301

A:Accession: A27622

A:Molecule type: mRNA

A:Residues: 1-58, 'T', '60-239 &lt;HUA&gt;

A:Accession: B27622

A:Molecule type: DNA

A:Note: the sequence was determined from the germline gene

C:Comment: Constitutive expression of Bcl2 following t(14;18) chromosomal translocation

C:Genetics:

A:Gene: GDB:BCL2

A:Cross-references: GDB:119031; OMIM:151430

A:Map position: 18q21.3-18q21.3

C:Function:

A:Description: blocks apoptosis in hematopoietic cells

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto

Query Match 7.8%; Score 116; DB 1; Length 239;

Best Local Similarity 19.4%; Pred. No. 0.0043;

Matches 48; Conservative 39; Mismatches 76; Indels 84; Gaps 10;

QY 79 DIEGFVVDFTIRIRONGMEW----- 100

DB 10 DNEIIVMKTIHYKLSQRGTEMDAGVCAAPGAPGIFSSPGHTPPAASRDEAVNT 69

QY 101 -----GAPGLPG-----VQ- EHEMRVMTIEFKKHAENFEFCEDLLAVPRISFSL 148

DB 70 SPLQTPAAGGAAGPALSPVPVHLTLRQAGDDFSRRYRDRFAEMSSQLHLTPFARGR 129

QY 149 YDQVATVCAQTDQCPMSYGRLLIGLISGCFVAAKMAESV--ELQGVARNLFTVTSLEFI 206

## RESULT 9

TVMSA1

transforming protein bcl-2-alpha - mouse

C:Species: Mus musculus (house mouse)

C&gt;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 18-Jun-1999

C:Accession: A25960; E37332

R:Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.

Cell 49, 455-463, 1987

A:Title: Molecular analysis of mbcl-2: structure and expression of the murine gene ho

A:Reference number: A90893; MUID:87187643; PMID:3032455

A:Accession: A25960

A:Molecule type: DNA

A:Residues: 1-236 &lt;NEG&gt;

A:Cross-references: GB:I31532; GB:M16506; NID:q468336; PIDN:AAA37282.1; PID:q387109

R:Enguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety

A:Reference number: A37332; MUID:92375724; PMID:1508712

A:Accession: E37332

A:Status: preliminary; nucleic acid sequence not shown: not compared with conceptual

A:Molecule type: DNA

A:Residues: 1-33, 'E', '34-220, 'AL', '223-236 &lt;EGU&gt;

C:Genetics:

A:Gene: BCL2

A:introns: 192/3

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

A:Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equivalent expression of bcl-2 and bcl-xl in granulosa cells and constitutive bcl-2 and bcl-xl in theca cells.  
 A:Reference number: 153295; PMID:95129487; PMID:7828536  
 A:Accession: 167432  
 A:Status: preliminary; translated from GR/EMBL/DBD  
 A:Molecule type: mRNA  
 A:Residues: 1-236 <RES>  
 A:Cross-references: EMBL:U03964; NID:g1004378; PIDN:AAA77687.1; PID:g1004379  
 C:Superfamily: bcl transforming protein

Db	69	TSPLRPVIANNGALSPVPVPHVHLTLRRAGDDFSRRRRDFAEMSSQHLHLPFTARGRA	128
Qy	151	DVPEVTGNAQIQDQCPMSYGRFLIGLISGCGVAAKMMESVLCQOVRLLFVYTSLEFKTRI	210
Db	129	TVVE-----ELFRDGVMMGRVAFEEFGGVCVGSVNR-EMSPVLDVIALMTEYLNRLH	182
Qy	211	RNNKKEHNRSDDEMTL-GKQMKEDYERAAEKVGRKKQNRW-----SMIGAVY	260
Db	183	HTVIQDNGGWDAEVLEYEGSMRPLPDFS-----WLSKTLTSLALVGACIT	228
Qy	261	AGA 263	
Db	229	LGA 231	

RESULT 14  
I49057  
bcl-x transmembrane deleted - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999  
C:Accession: I49057  
R:Feng, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.  
J. Immunol. 153, 4388-4398, 1994  
A:Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes  
A:Reference number: I49055; MUID:95052604; PMID:763517  
A:Accession: I49057  
A:Status: preliminary; translated from GB/EWML/DDJ3  
A:Molecule type: mRNA  
A:Residues: 1-214 <RES>  
A:Cross-references: EMBL:U0102; NID:g506649; PIDN:AAA82174.1; PID:g506650  
C:Genetics:  
A:Gene: bcl-x-long  
A:Superfamily: bcl transforming protein

Query Match	7.3%;	Score 108;	DB 2;	Length 214;
Best Local Similarity	19.2%;	Pred. No. 0.021;		
Matches 37;	Conservative 31;	Mismatches 65;	Indels 60;	Gaps 6;

  

QY	84	VVDYFTHIRONGMEF-----	CA	102
		: : : :		
Db	9	VDFLSYLSQSGYSQFSDVENRTEAPEETEARETPSA1NGNPSWHLDSAPVANG		68
QY	103	PGDLGVOPEH-----EMKRVNGTIFPEKKHAENFETFCOLLAVRISLSLVODVVR		154
		: : : : :   : : : :		
Db	69	TGHSSSLAREYIPAAVKQALREAGDEFELRRAFSDLSQHLTTFETAYQSEQVYN		128
QY	155	TVGNAQTDQCPMSYGLISLFGGVAAKMEYSV-ELQGOVRNRLPYTSLFIKTRIRN		212
		: : : : :   : : : :		
Db	129	-----ELPRDGVNMGRIVAFESFGS--ALCVESYDKEMQVLSRIASWMAATYINDHL-E		179
QY	213	NWKEHNRSDQDEM 225		
		: : : :   : : : :		
Db	180	PIQDENGSGDITFV 192		

RESULT 15  
AE1901  
WD-repeat containing protein [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp.  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002  
C:Accession: AE1901  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kunitz, T.; Sasamoto, S.; Watanabe, A.; Iriuguchi, S.; Tanaka, K.; Shimizu, K.; Takizawa, S.; Nakazaki, N.; Shimpō, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.; Nakazaki, N.; Shimpō, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.; Nakazaki, N.; Shimpō, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. strain PCC 7120  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AE1901  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1328 <KUR>  
A:Cross-references: GB:BA000019, PID:BA072716.1; PID:g17130104; GSPDB:GN00179

A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: al10759

Query Match 7.3%; Score 108; DB 2; Length 1329;  
Best Local Similarity 22.7%; Pred. No. 0.23;  
Matches 68; Conservative 39; Mismatches 101; Indels 92; Gaps 14;

OY	12	NPAVRRRMATGEKKEFLGIGTGPTEPDGLISNDQDPPSPROASTR--MSIGSI--	DG	68
		:   :		
Db	173	NPAKRLTFA-----LLGA-	-TPGDLDQTKTPPNIGALIEDG	2111
OY	69	K-INDWEEPRIDIEGFVVDFTTHIRONGHEWGEGAPLPCGVQ----		110
		:   :   :		
Db	212	FKIHDIETLAGLGAKVEN--PQAVMOEVLAMTG--CQPPLTQPVCELLKALSIEKRDP		267
OY	111	--PEHEMRMRYMGATIEFEKKHAENE-----TFCEOLLAAVPRI--FSLYQDVVRT		155
		: : : : :   :   :		
Db	268	RSYDENQIETLVKRETIHQIIDINEANDKOEHLKTIIDRLILISEISVALLGLXQQQLQQ		327
OY	156	VGNAGTDCCPMNSYGRLLIGLISFGSGFVAKKMESVELOGYVRNL-EVYTSLEFIKTIRINN-		213
		:   :   :   :   :		
Db	328	VMETADSSFEQMRLRTLNGIV-----VOOGKGLRVYNQIARYNEFDLSWEENEL		374
OY	214	-----MKEHNRSMDEFTLGKQMKEDERYERAEKVGRKRRNRRMSGTMGGVTA		261
		:   :   :		
Db	375	GKLAFYADKLRAWVESNTIQDTCLLWG---EDLERKRWAGDGKSLSDVDFRLISAIVEA		430

Search completed: February 24, 2003, 11:55:06  
Job time : 20 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 24, 2003, 11:51:39 ; Search time 11 seconds  
(without alignments)  
1055.761 Million cell updates/sec

Title: US-09-993-420A-3

Perfect score: 1479  
Sequence: 1 MTRCTADNLSLTNPATRRRTM.....AGAGTGVVCGRMFSLK 280

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1479	100.0	280	1	CEB9_CAEEL
2	898.5	60.8	271	1	CEB9_CAEEL
3	151	10.2	193	1	BCLW_MOUSE
4	150	10.1	193	1	BCLW_MOUSE
5	135	9.1	233	1	BCLX_HUMAN
6	135	9.1	233	1	BCLX_HUMAN
7	132	8.9	233	1	BCLX_MOUSE
8	131	8.9	233	1	BCLX_MOUSE
9	125.5	8.5	228	1	ARL_XENLA
10	118.5	8.0	226	1	BCL2_MOUSE
11	118	8.0	229	1	BCL2_MOUSE
12	116	7.8	233	1	BCL2_MOUSE
13	116	7.8	233	1	BCL2_MOUSE
14	114.5	7.7	236	1	BCL2_MOUSE
15	113.5	7.6	229	1	BCL2_MOUSE
16	112	7.6	177	1	BCL2_MOUSE
17	110.5	7.5	236	1	BCL2_MOUSE
18	95	6.4	350	1	BCL2_MOUSE
19	90	6.1	274	1	BCL2_MOUSE
20	89.5	6.1	1217	1	BCL2_MOUSE
21	88	5.9	436	1	BCL2_MOUSE
22	87	5.9	347	1	BCL2_MOUSE
23	86.5	5.8	358	1	BCL2_MOUSE
24	85	5.7	1788	1	BCL2_MOUSE
25	84	5.7	519	1	BCL2_MOUSE
26	83	5.6	361	1	BCL2_MOUSE
27	83	5.6	516	1	BCL2_MOUSE
28	83	5.6	545	1	BCL2_MOUSE
29	82.5	5.6	574	1	BCL2_MOUSE
30	82.5	5.6	852	1	BCL2_MOUSE
31	82	5.5	845	1	BCL2_MOUSE
32	81.5	5.5	418	1	BCL2_MOUSE
33	81.5	5.5	518	1	BCL2_MOUSE

34	81.5	5.5	661	1	DYN_DROME
35	81	5.5	391	1	Y532_METJA
36	81	5.5	515	1	NFED_BRAJA
37	81	5.5	528	1	ATPB_BOVIN
38	80	5.4	491	1	NFED_AZOVI
39	80	5.4	529	1	ATPB_HUMAN
40	79.5	5.4	372	1	RIBD_HAEIN
41	79.5	5.4	649	1	HEXB_STEIN
42	79.5	5.4	971	1	Y228_BORBU
43	79	5.3	604	1	PGH2_RAT
44	79	5.3	631	1	THIC_SALTY
45	79	5.3	639	1	BACQ_BACLI

## ALIGNMENTS

RESULT 1  
CEB9\_CAEEL STANDARD; PRT; 280 AA.  
ID CEB9\_CAEEL  
AC P41958:  
DT 01-NOV-1995 (rel. 32, last sequence update)  
DT 01-NOV-1995 (rel. 32, last sequence update)  
DT 15-JUN-2002 (rel. 41, last annotation update)  
DE Apoptosis regulator ced-9 (Cell death protein 9).  
GN CED-9 OR T07C4.8.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Pelodierinae; Caenorhabditis.  
OX NCBI\_TaxId=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Bristol N2;  
RX MEDLINE=94170367; PubMed=7907274;  
RA Hengartner M.O., Horvitz H.R.;  
RT "C. elegans cell survival gene ced-9 encodes a functional homolog of  
RL the mammalian proto-oncogene bcl-2.";  
RL Cell 76:665-676(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Bristol N2;  
RX Berks M., Durbin R.;  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP CHARACTERIZATION, AND MUTAGENESIS.  
RC STRAIN-Bristol N2;  
RX MEDLINE=97177114; PubMed=9024666;  
RA Specter M.S., Desnoyers S., Hoepfner D.J., Hengartner M.O.;  
RT "Interaction between the C. elegans cell-death regulators CED-9 and  
RL CED-4.";  
RL Nature 385:653-656(1997).  
CC -!- FUNCTION: CAN BOTH PROMOTE AND PREVENT PROGRAMMED CELL DEATH  
CC (APOPTOSIS) WHICH IS ESSENTIAL FOR DEVELOPMENT AND HOMEOSTASIS. IT  
CC DOES THIS BY ANTAGONIZING THE DEATH PROMOTING/PREVENTING  
CC ACTIVITIES OF CED-3, CED-4S AND CED-4L. IT BINDS STRONGLY TO CED-  
CC 4S AND LESS SO TO CED-4L.  
CC -!- DEVELOPMENTAL STAGE: ABUNDANT EXPRESSION IS SEEN IN THE EMBRYOS  
CC AND THE ADULTS.  
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC EMBL: L26545; AAA20080.1; -  
CC EMBL: Z29443; CAA82573.2; -  
DR

DR WormPep; T07C4.8; CE00599.  
 DR Interpro: IPR002475; BCL2\_family.  
 DR Interpro: IPR000712; Bcl2\_BH.  
 DR Interpro: IPR003093; Bcl2\_BH4.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; FALSE\_NEG.  
 DR PROSITE: PS01258; BH2; FALSE\_NEG.  
 DR PROSITE: PS01260; BH4\_1; FALSE\_NEG.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 DR Apoptosis.  
 KW Apoptosis.  
 FT DOMAIN 80 99 BH4.  
 FT DOMAIN 160 179 BH1.  
 FT DOMAIN 213 229 BH2.  
 FT MUTAGEN 149 149 Y->N: IN N1653; LETHAL PHENOTYPE.  
 FT MUTAGEN 169 169 G->E: IN G169E; GAIN OF FUNCTION.  
 SQ SEQUENCE 280 AA; 31824 MW; 7603675E490DD3EB CRC64;

Query Match 100.0%; Score 1479; DB 1; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 1,4e-126;  
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTRCTADNSTLTNPAYRRRTMATGEMKEFLGKTEPTFGINSADADLPSPROASTRRM 60  
 DB 1 MTRCTADNSTLTNPAYRRRTMATGEMKEFLGKTEPTFGINSADADLPSPROASTRRM 60  
 OY 61 SIGESIDGKINDMEEPRLDIEGFVVDYFTHIRIRONGEMWFGAGLPGVQPEHEMMRVNG 120  
 DB 61 SIGESIDGKINDMEEPRLDIEGFVVDYFTHIRIRONGEMWFGAGLPGVQPEHEMMRVNG 120  
 OY 121 TIFEKKAENFETFCEDLLAVPRISFSLYODVVRTVGNQATDQCPMSYGLIGLISFGFG 180  
 DB 121 TIFEKKAENFETFCEDLLAVPRISFSLYODVVRTVGNQATDQCPMSYGLIGLISFGFG 180  
 OY 181 VAAKMEVSVALQGVNLFYVTSLFITKTRIRNNKKEHNSWDDEFTMLGKQMKEDYERABA 240  
 DB 181 VAAKMEVSVALQGVNLFYVTSLFITKTRIRNNKKEHNSWDDEFTMLGKQMKEDYERABA 240  
 OY 241 EKYGRKRRKRRMSMIGAGVTAGATGIVGVVCGRRMPSLK 280  
 DB 241 EKYGRKRRKRRMSMIGAGVTAGATGIVGVVCGRRMPSLK 280

RESULT 2  
 CED9\_CAEBR  
 ID CED9\_CAEBR STANDARD; PRT: 271 AA.  
 AC P41957;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator ced-9 (Cell death protein 9).  
 GN CED-9.  
 OS Caenorhabditis briggsae.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea;  
 OC Rhabdilitidae; Rhabdilitinae; Caenorhabditis.  
 ON NCBI\_TaxID=6238;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94170367; PubMed=7907274;  
 RA Hengartner M.O., Horvitz H.R.;  
 RT "C. elegans cell survival gene ced-9 encodes a functional homolog of  
 RT the mammalian proto-oncogene bcl-2.";  
 RL Cell 76:665-676(1994).  
 CC -I- FUNCTION: PROTECT CELLS THAT NORMALLY SURVIVE FROM UNDERGOING  
 CC PROGRAMMED CELL DEATH (APOPTOSIS) WHICH IS ESSENTIAL FOR  
 CC DEVELOPMENT AND HOMEOSTASIS.  
 CC -I- DEVELOPMENTAL STAGE: ABUNDANT EXPRESSION IS SEEN IN THE EMBRYOS  
 CC AND THE ADULTS.  
 CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.

CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -I- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
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DR EMBL: L26546; AAA20077.1;  
 DR Interpro: IPR002475; BCL2\_family.  
 DR Interpro: IPR000712; Bcl2\_BH.  
 DR Interpro: IPR003093; Bcl2\_BH4.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; FALSE\_NEG.  
 DR PROSITE: PS01258; BH2; FALSE\_NEG.  
 DR PROSITE: PS01260; BH4\_1; FALSE\_NEG.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 DR Apoptosis.  
 KW Apoptosis.  
 FT DOMAIN 80 99 BH4.  
 FT DOMAIN 159 179 BH1.  
 FT DOMAIN 213 228 BH2.  
 SQ SEQUENCE 271 AA; 31214 MW; CDC135B0C539201F CRC64;

Query Match 60.8%; Score 898.5; DB 1; Length 271;  
 Best Local Similarity 60.8%; Pred. No. 4.7e-74;  
 Matches 178; Conservative 34; Mismatches 45; Indels 17; Gaps 6;

OY 8 NSLTNPATRRRTMATGEMKEFLGKTEPTFGINSADADLPSPROASTRRMSSTESTI 66  
 DB 14 NSSQN-TFRRTMATSEKREFLSTKDAEPNFGM---QRTIESPTSTPTRRMSIDST 68  
 OY 67 DGIKINDMEEPRLDIEGFVVDYFTHIRIRONGEMWFGAGLPGVQPEHEMMRVNGTITEKK 126  
 DB 69 ---RIYDMEEPRLDIEGFVVDYFTHIRIRONGEMWFGAGLPGVQPEHEMMRVNGTITEKK 126  
 OY 127 HAENFETFCEDLLAVPRISFSLYODVVRTVGNQATDQCPMSYGLIGLISFGFGVAAKM 186  
 DB 127 HMEFENFSEQLLAVPRISFSLYODVVRTVGNQATDQCPMSYGLIGLISFGFGVAAKM 186  
 OY 187 ESVELQGVNLFYVTSLFITKTRIRNNKKEHNSWDDEFTMLGKQMKEDYERAEKYGRR 246  
 DB 187 ESVELQGVNLFYVTSLFITKTRIRNNKKEHNSWDDEFTMLGKQMKEDYERAEKYGRR 246  
 OY 247 KÖNRRMSMIGAGVTAGATGIVGVVCGRRMPSLK 280  
 DB 247 LKS--WSITGASV-----IAVTCGRILIFSPK 271

RESULT 3  
 BCLW\_MOUSE  
 ID BCLW\_MOUSE STANDARD; PRT: 193 AA.  
 AC P70345;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-W.  
 GN BCL2L2 OR BCLW.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96358615; PubMed=8761287;  
 RA Gibson L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,  
 RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;



"bcl-w, a novel member of the bcl-2 family, promotes cell survival.";  
 RL Oncogene 13:665-675(1996).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=C57BL/10J;  
 RX MEDLINE=98160183; PubMed=9500547;  
 RA Ross A.J., Maynair K.G., Moss J.E., Parlow A.F., Skinner M.K.,  
 Russell L.D., Macgregor G.R.,  
 RT "testicular degeneration in Bclw-deficient mice.";  
 RL Nat. Genet. 18:251-256(1998).  
 CC -1- FUNCTION: PROMOTES CELL SURVIVAL.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND  
 CC IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,  
 CC AND SALIVARY GLAND.  
 CC -1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC  
 CC FUNCTION.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: U59746; AAB09056.1; -;  
 DR EMBL: AF030769; AAB86430.1; -;  
 DR HSSP: Q07817; IMAZ.  
 DR MGD: MGI:108052; Bcl2l2.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH4.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01260; BH4\_1; 1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 DR Apoptosis.  
 KW Apoptosis.  
 FT DOMAIN 9 29 BH4.  
 FT DOMAIN 85 104 BH1.  
 FT DOMAIN 136 151 BH2.  
 SQ SEQUENCE 193 AA; 20790 MW; 36CA185F5945DFB4 CRC64;

Query Match 10.2%; Score 151; DB 1; Length 193;  
 Best Local Similarity 24.3%; Pred. No. 1.4e-06;  
 Matches 51; Conservative 31; Mismatches 92; Indels 36; Gaps 8;

QY 79 DIEGIVNDFTRIRNGEMHMGARGLPCGVQPEHEHMKVMTIEKKHAENFEFCQL 138  
 DB 9 DTRALVADVFYKLRKGVGCGAGPEGPADPLDQAKMAAGDEDETRRRRFFSLAOL 68  
 QY 139 LAVP-----RISFSLQDVVTRVGNATQDCPMSTYGRLLGLISFGGFAAKM--ES 188  
 DB 69 HTYFGAQRFTQVSDLEFG-----GPMNGRLVAFFVFAGALCAESVKNEM 115  
 QY 189 VELQGVNRLFYVTSLEFTRIRNNKKEHNSWDEMTLTKOMKEDYEAEKVGRRQ 248  
 DB 116 EPLVGVQVDMV---AYLETRILA-DWIHSSGMAEFTAL-----YDGALEE-ARRLR 163  
 QY 249 NRRWSMIGAGTAGIAGIIVGAVVCGRMFS 278  
 DB 164 EGNMVASVRT-VLTGAVALGALTVGCAFFAS 192

RESULT 4  
 BCLW\_HUMAN STANDARD; PRT; 193 AA.  
 ID BCLW\_HUMAN  
 AC 092843;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-w.  
 GN BCL2L2 OR BCLW OR KIAA0271.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96358615; PubMed=8761287;  
 RA Gibson L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,  
 RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;  
 RT "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";  
 RL Oncogene 13:665-675(1996).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Brain;  
 RX MEDLINE=97191544; PubMed=9039502;  
 RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayashi Y.,  
 RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;  
 RT Prediction of the coding sequences of unidentified human genes. VI.  
 RT The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by  
 RT analysis of cDNA clones from cell line K5-1 and brain.";  
 RL DNA Res. 3:321-329(1996).  
 CC -1- FUNCTION: PROMOTES CELL SURVIVAL.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND  
 CC IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,  
 CC AND SALIVARY GLAND.  
 CC -1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC  
 CC FUNCTION.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
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 CC -----  
 DR EMBL: U59747; AAB09055.1; -;  
 DR EMBL: D87461; BAA19666.1; -;  
 DR HSSP: Q07817; IMAZ.  
 DR Genew: HGNC:995; BCL2L2.  
 DR MIM: 601931; -;  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH4.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01260; BH4\_1; 1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 DR Apoptosis.  
 KW Apoptosis.  
 FT DOMAIN 9 29 BH4.  
 FT DOMAIN 85 104 BH1.  
 FT DOMAIN 136 151 BH2.  
 SQ SEQUENCE 193 AA; 20774 MW; 3792243A50281761 CRC64;

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Query Match Similarity      10.1%; Score 150; DB 1; Length 193;
Best Local Similarity      24.3%; Pred. NO.1.7e-06;
Matches    51; Conservative   30; Mismatches   93; Indels    36; Gaps     8;

OY 79 DIEGFVVDYFTHIRONGEMWFGADQLPCGVOPPEHEMMKRWKTOTIEKKHAENFEFFCEOL 138
   | : : : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
DB 9 DTRALVADEVGKLRQKGVCAGCGEGCPAADPLHQAAMAGDEDEFETRRRFFSOLAOL 68

OY 139 LAVP-----RISESIXODVVRIVGNANQTDOCCMSXGRLLIGLISFGFAAKMM--ES 188
   | : : : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
DB 69 HVTPOSAQRFPFOVSDELFG--G-----GPNMGRLAFFFVFGLALCAESVNREM 115

OY 189 VELQGOVRNLFFYTSLFTKITRNNKEHNRSMDPEMTLGKOMKEDYEAEAEKYGRRKO 248
   ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
DB 116 EPLVGYOVGEVMV---AYLETRLA-DWIHSNGMAEFTL-----YDGLALEF-ARRLR 163

OY 249 NRRSMICAGVYAGAIIGIVGVYGCRRMFS 278
DB 164 EGNMASVRT-VLTGAVALGALTATGAFRAS 192

RESULT 5
BCI_X_HUMAN
ID BCI_X_HUMAN STANDARD: PRT: 233 AA.
AC 007817; Q92976;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-x.
GN BCL2L1 OR BCL2L1L OR BCLXL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
[1]
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RX MEDLINE=93364977; PubMed=8358789;
RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator
RT of apoptotic cell death."
RT Cell 74:597-608(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RA Inohara N., Ohta S.;
RX submitted (Oct-1996) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION.
RX MEDLINE=95372373; PubMed=7644501;
RA Szelak T.W., Olvtai Z.N., Yang E., Wang K., Boise L.H., Thompson C.B.,
RA Korsmeyer S.J.;
RT "Multiple Bcl-2 family members demonstrate selective dimerizations
RT with Bax."
RT Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995).
RN [4]
RP MUTAGENESIS OF BH1 AND BH2 DOMAINS.
RX MEDLINE=96170038; PubMed=8596636;
RA Cheng E.H.-Y., Levine B., Boise L.H., Thompson C.B., Hardwick J.M.,
RA Korsmeyer S.J.;
RT "Bax-independent inhibition of apoptosis by Bcl-XL."
RT Nature 379:554-556(1996).
RN [5]
RP STRUCTURE BY NMR OF 1-209.
RX MEDLINE=97172562; PubMed=9020082;
RA Settler M., Liang H., Nettlesheim D., Meadows R.P., Harlan J.E.,
RA Ederstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,
RA Thompson C.B., Fesik S.W.;
RT "Structure of Bcl-XL-Bak peptide complex: recognition between
RT regulators of apoptosis."
RT Science 275:983-986(1997).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209.
RX MEDLINE=96256675; PubMed=8692227;

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CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
DR EMBL: X83574; CAAS8557.1; -
DR EMBL: L35049; AAA51039.1; -
DR EMBL: L35048; AAA51040.1; -
DR EMBL: U10102; AAA82174.1; -
DR EMBL: U10101; AAA82173.1; -
DR EMBL: U10100; AAA82172.1; -
DR EMBL: U51279; AAC53460.1; -
DR EMBL: U78031; AAB96881.1; -
DR EMBL: U78030; AAB96881.1; JOINED.
DR HSSP: P53563; IAP3.
DR MGD: MGI:88139; BCL2L1.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2_BH.
DR InterPro: IPR003093; BCL2_BH4.
DR InterPro: IPR004725; BCL2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRFAMs: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4; 1; 1.
DR PROSITE: PS50063; BH4_2; 1.
DR Apoptosis; Mitochondrion; Alternative splicing; Transmembrane.
KW
FT DOMAIN 4 24
FT DOMAIN 8 100
FT DOMAIN 129 148
FT DOMAIN 180 195
FT TRASMEM 210 226
FT VARSPIC 126 188
FT VARSPIC 189 233
FT VARSPIC 194 233
FT VARSPIC 233 233
FT SEQUENCE 233 AA; 26132 MW; 24D2AC79887E072E CRC64;
Query Match 8.9%; Score 132; DB 1; Length 233;
Best Local Similarity 20.9%; Pred. No. 9.2e-05;
Matches 52; Conservative 39; Mismatches 82; Indels 76; Gaps 10;

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Db 226 LG-SLFSRK 233
|:|:|
RESULT 8
BCLX_PIG ID BCLX_PIG STANDARD; PRT; 233 AA.
AC 077737;
DT 15-JUL-1999 (rel. 38, Created)
DT 15-JUN-1999 (rel. 38, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-x.
GN BCL2L1 OR BCL2L OR BCLX.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP MEDLINE=99171363; PubMed=10072723;
RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RT "Quantification of cardioprotective gene expression in porcine
RT short-term hibernating myocardium."
RL J. Mol. Cell. Cardiol. 31:147-158(1999).
CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of
CC caspases (By similarity). Appears to regulate cell death by
CC blocking the voltage-dependent anion channel (VDAC) by binding
CC to it and preventing the release of the caspase activator,
CC cytochrome c, from the mitochondrial membrane.
CC -1- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC similarity). Heterodimerization with BAX does not seem to be
CC required for anti-apoptotic activity (By similarity).
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE AND PERINUCLEAR
CC ENVELOPE (By similarity).
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC The BH1 and BH2 domains are required for both heterodimerization
CC with other Bcl2 family members and for repression of cell death.
CC -1- PTM: Proteolytically cleaved by caspases during apoptosis (By
CC similarity). The cleaved protein, lacking the BH4 domain, has pro-
CC apoptotic activity (By similarity).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AJ001203; CAA04597.1; -
DR HSSP: Q07817; IMAZ.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2_BH.
DR InterPro: IPR003093; BCL2_BH4.
DR InterPro: IPR004725; BCL2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRFAMs: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4; 1.
DR PROSITE: PS50063; BH4_2; 1.
DR Apoptosis; Mitochondrion; Transmembrane.
KW
FT DOMAIN 4 24
FT DOMAIN 8 100

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FT DOMAIN 86 100 BH3.  
 FT DOMAIN 129 148 BH1.  
 FT DOMAIN 180 195 BH2.  
 FT TRANSMEM 210 226 POTENTIAL.  
 SQ SEQUENCE 233 AA; 26061 MW; 18BF6FA0441912B2 CRC64;

Query Match 8.9%; Score 131; DB 1; Length 233;  
 Best Local Similarity 20.9%; Pred. No. 0.00011;  
 Matches 52; Conservative 39; Mismatches 82; Indels 76; Gaps 10;

QY 84 VVDYFTHRIKRGKMEWF-----GAPGLPCGVOPHE----- 114  
 DB 9 VVDFTSKYKSGKGYNSQPTDVEENKTEPECTESEAETPPALNGNPSMHLADSPAVNGA 68  
 QY 115 -----NMKVGITFEKKHAENFTFCGOLLAVPRISFLYQDVVR 154  
 DB 69 TGHSSSLDAREVYPMAAVYQALREAGDEDELATYRAFSDLISQLHTPTGTAVQSEGYLN 128  
 QY 155 TVGNMOTQCPMSYGRLLIGLSFGGFVAAKMMESV--ELQGVNRLFYVTSLEFKTRIRN 212  
 DB 129 -----ELFPDGVNMGRIYAFVFEFG--ALCVESYDKEMOVLVSRIATMATYINDHL-E 179  
 QY 213 NMKEHNRSWDDPMTLGKQMKEDY-ERAEAEKVRKRRKRRSMIGAGVTAGAIQVGVV 271  
 DB 180 PWIQNGMGDPFVEL-----YGNMAAESEKRGGERNNRFLTG-----MTLAGVVL 225  
 QY 272 CGRMFSLK 280  
 DB 226 LG-SLEFSRK 233

## RESULT 9

ARL\_XENLA

ID ARL\_XENLA STANDARD; PRT; 228 AA.

AC Q91827;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator R1 (XRL) (Fragment).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 CC Xenopodidae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Head;  
 RX MEDLINE=95331613; PubMed=7607538;  
 RA Cruz-Reyes J., Tata J.R.;  
 RT "Cloning, characterization and expression of two Xenopus bcl-2-like  
 cell survival genes."  
 RL Gene 158:171-179(1995).  
 CC -1- FUNCTION: COULD BE THE HOMOLOG OF MAMMALIAN BCL-W.  
 CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).  
 CC -1- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE  
 CC BRAIN OF MID-METAMORPHOSIS TO POST-METAMORPHOSIS TADPOLES AND  
 CC ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
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DR EMBL: X82462; CA57845.1; -;  
 DR HSSP: Q07817; IMA2.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; Bcl2\_BH.

DR InterPro: IPR003093; Bcl2\_BH4.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS5062; BCL2\_FAMILY; 1.  
 KW Apoptosis; Transmembrane.  
 FT NON\_TER 1  
 FT DOMAIN 120 139 BH1.  
 FT DOMAIN 171 186 BH2.  
 FT TRANSMEM 207 227 POTENTIAL.  
 SQ SEQUENCE 228 AA; 25068 MW; C499D449A585F8A9 CRC64;

Query Match 8.5%; Score 125.5; DB 1; Length 228;  
 Best Local Similarity 21.7%; Pred. No. 0.00035;  
 Matches 44; Conservative 44; Mismatches 92; Indels 23; Gaps 8;

QY 78 LDIEGFVVDYFTHRIKRGKMEWFGAPGLPCGVOPHEHMRVMGTIFEKKHAENFTFCQ 137  
 DB 46 LGSRALVEDLVRYKLCQRSLLVPEPSGASCAL---HSARAGADEFEKFRQAFSEISTQ 102  
 QY 138 LLAVERISESLYQDVVTVGNMOTQCPMSYGRLLIGLSFGGFVAAKMMESV--ELQGV 195  
 DB 103 IHVTPGTAYARFAFEVAGSL-----FOGVNMGRIYAFVFEFG--ALCAESYVKKEMSPIL 154  
 QY 196 RNLFVYTSLEFKTRIRNNKMEHNRSWDDPMTLGKQMKEDYERAEAKVRKRRKRRSMI 255  
 DB 155 PRIQDMWVYLETNLR-DWIQSNGWNGFLTL-----YGDGAIBE-AROREGNWASL 205  
 QY 256 GAGVTAGAIQVGVVCGRMFS 278  
 DB 206 KT-VLTGAVALGALMTVGALFAS 227

## RESULT 10

BCL2\_MOUSE

ID BCL2\_MOUSE STANDARD; PRT; 236 AA.

AC P10417; P10418;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2 OR BCL-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
 RC STRAIN=BALB/C; TISSUE=Liver;  
 RX MEDLINE=87187643; PubMed=3032455;  
 RA Negini M., Sillim E., Kozak C., Tsujimoto Y., Croce C.M.;  
 RT "Molecular analysis of mbcl-2: structure and expression of the murine  
 RT gene homologous to the human gene involved in follicular lymphoma.";  
 RL Cell 49:455-463(1987).  
 CC [2]  
 CC REVISIONS TO 221-222.  
 RX MEDLINE=92375724; PubMed=1508712;  
 RA Egnuchi Y., Ewert D.L., Tsujimoto Y.;  
 RT "Isolation and characterization of the chicken bcl-2 gene: expression  
 RT in a variety of tissues including lymphoid and neuronal organs in  
 RT adult and embryo."  
 RL Nucleic Acids Res. 20:4187-4192(1992).  
 RN [3]  
 RP PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.  
 RX MEDLINE=97277291; PubMed=9115213;  
 RA Ito T., Deng X., Carr B., May W.S., Jr.;  
 RT "Bcl-2 phosphorylation required for anti-apoptosis function.";  
 RL J. Biol. Chem. 272:11671-11673(1997).  
 RN [4]  
 RP DEPHOSPHORYLATION BY PP2A.

RX MEDLINE=99069407; PubMed=9852076;  
 RA Deng X., Ito T., Carr B., Mummy M., May W.S. Jr.;  
 RT "Reversible phosphorylation of Bcl2 following interleukin 3 or  
 RT bryostatin 1 is mediated by direct interaction with protein  
 RT phosphatase 2A\*";  
 RU J. Biol. Chem. 273:34157-34163(1998).  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 CC including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (APAF-1).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2  
 CC domains, and is necessary for anti-apoptotic activity (By  
 CC similarity). Also interacts with APAF-1 and RAFF-1.  
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 CC membrane of the nuclear envelope and the endoplasmic reticulum.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: alpha (shown here) and beta.  
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues.  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
 CC for interaction with RAFF-1.  
 CC -1- PHOSPHORYLATION/DEPHOSPHORYLATION ON Ser-70 regulates Bcl2  
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and  
 CC occurs during the G2/M phase of the cell cycle. In the absence of  
 CC growth factors, Bcl2 appears to be phosphorylated by other protein  
 CC kinases such as ERKs and stress-activated kinases.  
 CC Dephosphorylated by protein phosphatase 2A (PP2A).  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 CC activity, causes the release of cytochrome c into the cytosol  
 CC promoting further caspase activity.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: L31532; AAA37282.1; -;  
 DR EMBL: M16506; AAA37282.1; JOINED.  
 DR EMBL: M16506; AAA37281.1; -;  
 DR PIR: A25960; TVMSA1.  
 DR PIR: B25960; TVMSA1.  
 DR PIR: E37332; E37332.  
 DR HSSP: 007817; 1MAZ.  
 DR MGD: MGI:88138; Bcl2.  
 DR InterPro: IPR002473; BCL2\_family.  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR003093; BCL2\_BH4.  
 DR InterPro: IPR004725; BCL2-reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRFAMs: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS00062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4\_1; 1.  
 DR PROSITE: PS01260; BH4\_1; 1.  
 DR PROSITE: PS00063; BH4\_2; 1.  
 KW Apoptosis; Alternative splicing; Transmembrane; Mitochondrion;

KW Phosphorylation.  
 FT DOMAIN 10 30 BH4.  
 FT DOMAIN 90 104 BH3.  
 FT DOMAIN 133 152 BH1.  
 FT DOMAIN 184 199 BH2.  
 FT TRANSMEM 209 230 POTENTIAL.  
 FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).  
 FT MOD\_RES 70 70 PHOSPHORYLATION (BY PKC).  
 FT VARSLIC 193 236 DAFVLYGSPMRPLDFEWSLTKLTLALVAGCTTGAVL  
 FT VARSPLIC 193 236 GHK -> VGACTIVE (IN ISOFORM BETA).  
 SQ SEQUENCE 236 AA; 26425 MW; AA85EF6B0766BE0A CRC64.  
 Query Match 8.0%; Score 118.5; DB 1; Length 236;  
 Best Local Similarity 20.0%; Pred. No. 0.0016;  
 Matches 49; Conservative 40; Mismatches 73; Indels 83; Gaps 11.  
 QY 79 DIEGFVVDYFTNRIRONGMEW-----FGA---PGLPCGVDP----- 112  
 DB 10 DNREIWMKYHYKLSORGYEMDAGDADAPLGAAPPGI-FSPQSPNDMPVHREMAR 68  
 QY 113 -----HEMRYVGTIFEKKHANFETFCQLAVPRISFLYQ 150  
 DB 69 TSPRLPLVATAGALSPVPCVHLTLRRAGDDFSRRYRRDPFAMSSQLHFTTARGRA 128  
 QY 151 DVYRTVGNAGTDDCPMSYGRILGLISGGEFVAAKMEV--ELGGVNRLLFVYTSLEFT 208  
 DB 129 TVVE-----ELFRDGVNMGWRIYVFEFGVWC---VESVNRKMSPLVDNALMFTYLR 180  
 QY 209 RIRNNKEHNRSSDDFTWL-GKQMKEDYERAEKVKRQRNRW-----SMIGAG 258  
 DB 181 HL-HTWIQDNGMDAFVLYGSPMRPLDFES-----WLSLTKLTLALVAGC 226  
 QY 259 VTAGA 263  
 DB 227 ITLGA 231  
 RESULT 11  
 BCL2\_BOVIN STANDARD; PRT; 229 AA.  
 ID BCL2\_BOVIN  
 AC 002718;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_Taxid=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Holstein; TISSUE=thymus;  
 RA Reyes R.A., Cockrell G.L.;  
 RT "Bovine leukemia virus associated-leukemogenesis is correlated  
 RT with suppression of programmed cell death and increased expression  
 RT of Bcl-2";  
 RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 CC including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (APAF-1) (By similarity).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2  
 CC domains, and is necessary for anti-apoptotic activity (By  
 CC similarity). Also interacts with APAF-1 and RAFF-1 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 CC membrane of the nuclear envelope and the endoplasmic reticulum (By  
 CC similarity).





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DR HSP: Q07817.1MAZ. BCL2_family.
DR InterPro: IPR002475; BCL2_BH.
DR InterPro: IPR000712; BCL2_BH.
DR InterPro: IPR003093; BCL2_BH4.
DR InterPro: IPR004725; BCL2-reg.
DR Pfam: PF00452; BCL-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRFAMs: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PS50063; BH4_2; 1.
DR Apoptosis; Transmembrane; Mitochondrion.
KW DOMAIN 10 30 BH4.
FT DOMAIN 87 101 BH3.
FT DOMAIN 130 149 BH1.
FT DOMAIN 181 196 BH2.
FT TRANSMEM 208 228 POTENTIAL.
FT TRANSMEM 64 64 E -> S (IN REF. 2).
FT CONFLICT 67 82 GSAAAEVPPAEGLRP -> ARLLVRCPLRGCA
FT CONFLICT (IN REF. 2).
FT CONFLICT 121 121 H -> T (IN REF. 2).
FT CONFLICT 139 139 G -> V (IN REF. 2).
SQ SEQUENCE 233 AA; 25687 MW; 5252555ACB6E4C3D CRC64;

Query Match
Best Local Similarity 19.9%; Score 116; DB 1; Length 233;
Matches 48; Conservative 38; Mismatches 77; Indels 78; Gaps 11;

QY 79 DIEGVYVDFTHRIKONGMEVFC-----APGLPC----- 107
| : : : : : |
DB 10 DNEIYLKYLHYKLSQGYDMAAGEDRPVPPAPAAAPAAAGASSHRRPEPGSA 69
| : : : : : |
QY 108 -----GVQPE-----DEMRVMTGTEKKHAENEFECBOLLAVPISFLYQDVYR 154
| : : : : : |
DB 70 AASEVPASGLRPPAPGVHIALKQACDEFSSRKQDFQAFMSQGLHLP---FTAHREPA 126
| : : : : : |
QY 155 TVGNAOTDCCPMISYGRLLIGLISFGFVAAKMMESV---ELQGOVRLNLFVYTSLEIKTRIRN 212
| : : : : : |
DB 127 VVELELRD--GVNMGRIIVAFPEFGVWC--VESVNRKSPVLDNATWMTXNLNHL-H 180
| : : : : : |
QY 213 NKEHNRSMDEFTL-GKQMKEDYEAEAEKVRKQNRW-----SMAGVYTG 262
| : : : : : |
DB 181 NMIDNGMDAFVELYGNMKRPLDPS-----WISLKTITSLVLVAGACITLG 227
| : : : : : |
QY 263 A 263
DB 228 A 228

```

RESULT 13  
BCL2\_HUMAN STANDARD: PRT; 239 AA.

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ID BCL2_HUMAN STANDARD: PRT; 239 AA.
AC P10415; P10416; Q16197; Q13842;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RX MEDLINE=86259760; PubMed=3523487;
RA Tsujimoto Y., Croce C.M.;
RT "Analysis of the structure, transcripts, and protein products of
RT bcl-2, the gene involved in human follicular lymphoma.";
```

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RL Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
RN [2]
RP REVISIONS TO 96; 110 AND 237.
RX MEDLINE=92375724; PubMed=1508712;
RA Echigi Y., Ewert D.L., Tsujimoto Y.;
RT "Isolation and characterization of the chicken bcl-2 gene: expression
RT in a variety of tissues including lymphoid and neuronal organs in
RT adult and embryo."
RL Nucleic Acids Res. 20:4187-4192(1992).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=88196071; PubMed=2834197;
RA Seto M., Jaeger U., Hockett R.D., Granlinger W., Bennett S.,
RA Goldman P., Korsmeyer S.J.;
RT "Alternative promoters and exons, somatic mutation and deregulation
RT of the Bcl-2-Ig fusion gene in lymphoma."
RL EMBO J. 7:123-131(1988).
RN [5]
RP SEQUENCE OF 1-131 FROM N.A. (ISOFORM ALPHA), AND VARIANTS NHL.
RX MEDLINE=92096610; PubMed=1339299;
RA Tanaka S., Louie D.C., Kant J.A., Reed J.C.;
RT "Frequent incidence of somatic mutations in translocated BCL2
RT oncogenes of non-Hodgkin's lymphomas."
RL Blood 79:229-237(1992).
RN [6]
RP SUBCELLULAR LOCATION.
RX MEDLINE=91069924; PubMed=2250705;
RA Hockenbery D., Nunez G., Millman C., Schreiber R.D., Korsmeyer S.J.;
RT "Bcl-2 is an inner mitochondrial membrane protein that blocks
RT programmed cell death."
RL Nature 348:334-336(1990).
RN [7]
RP MUTAGENESIS.
RX MEDLINE=94239528; PubMed=8183370;
RA Yin X.-M., Oltvai J.N., Korsmeyer S.J.;
RT "Bcl-2 and Bcl-2 are required for inhibition of
RT apoptosis and heterodimerization with Bax."
RL Nature 369:321-323(1994).
RN [8]
RP CLEAVAGE BY CASPASES, AND MUTAGENESIS.
RX MEDLINE=98057466; PubMed=9395403;
RA Cheng E.H.-Y., Kirsch D.G., Clem R.J., Ravi R., Kastan M.B., Bedi A.,
RA Ueno K., Hardwick J.M.;
RT "Conversion of Bcl-2 to a Bax-like death effector by caspases."
RL Science 278:1966-1968(1997).
RN [9]
RP REVIEW ON PHOSPHORYLATION.
RX MEDLINE=21260650; PubMed=11368354;
RA Ruvoilo P.P., Deng X., May W.S.;
RT "Phosphorylation of Bcl2 and regulation of apoptosis."
RL Leukemia 15:515-522(2001).
RN [10]
RP PHOSPHORYLATION BY ASK1/JNK1.
RX MEDLINE=20036804; PubMed=10567572;
RA Yamamoto K., Ichijo H., Korsmeyer S.J.;
RT "Bcl-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal
RT protein kinase pathway normally activated at G(2)/M."
RL Mol. Cell. Biol. 19:8469-8478(1999).
RN [1]
RP FUNCTION: Suppresses apoptosis in a variety of cell systems
CC including factor-dependent lymphohematopoietic and neural cells.
CC Regulates cell death by controlling the mitochondrial membrane
CC permeability. Appears to function in a feedback loop system with
CC caspases. Inhibits caspase activity either by preventing the
CC release of cytochrome c from the mitochondria and/or by binding to
CC the apoptosis-activating factor (Apaf-1).
```

```

CC -1 SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC domains, and is necessary for anti-apoptotic activity (By
CC similarity). Also interacts with APAF-1 and RAf-1.
CC -1 SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum.
CC -1 ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta;
CC are produced by alternative splicing.
CC -1 TISSUE SPECIFICITY: Expressed in a variety of tissues.
CC -1 DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RAf-1.
CC -1 PPM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle. In the absence of
CC growth factors, Bcl2 appears to be phosphorylated by other protein
CC kinases such as ERKs and stress-activated kinases.
CC -1 PPM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity.
CC -1 DISEASE: Involved in follicular lymphoma (FL) (also known as type
CC t(14;18)(q32;q21) which involves Bcl2 and immunoglobulin gene
CC regions.
CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1 DATABASE: NAME-Atlas Genet. Cytoenet. Oncol. Haematol.;
CC WWW:"http://www.infobiogen.fr/services/chromocancer/genes/BCL2ID49.html".
CC
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CC -----
CC EMBL: M13994; AAA51813.1; ALT_SEQ.
CC EMBL: M13995; AAA51814.1; ALT_SEQ.
CC EMBL: M14745; AAA35591.1; -.
CC EMBL: X06487; CA29778.1; -.
CC EMBL: S72602; AAD1411.1; ALT_SEQ.
CC PIR: A29409; TVH0A1.
CC PIR: B29409; TVH0B1.
CC PIR: A24428; TVH0BC.
CC PIR: C37332; C37332.
CC PIR: D37332; D37332.
CC HSSP: Q07817; IMAZ.
CC Genew: HGNC:990; BCL2.
CC MIM: 151430; -.
CC InterPro: IPR002475; BCL2 family.
CC InterPro: IPR000712; Bcl2_BH.
CC InterPro: IPR003093; Bcl2_BH4.
CC InterPro: IPR004725; Bcl2_Reg.
CC Pfam: PF00452; Bcl-2; 1.
CC Pfam: PF02180; BH4; 1.
CC SMART: SM00337; BCL; 1.
CC SMART: SM00265; BH4; 1.
CC TIGRfams: TIGR00865; bcl-2; 1.
CC PROSITE: PSS0062; BCL2_FAMILY; 1.
CC PROSITE: PS01080; BH1; 1.
CC PROSITE: PS01258; BH2; 1.
CC PROSITE: PS01259; BH3; 1.
CC PROSITE: PS01260; BH4_1; 1.
CC PROSITE: PSS0063; BH4_2; 1.
CC Proto-oncogene; Apoptosis; Alternative splicing; Transmembrane;
CC Mitochondrion; Phosphorylation; Chromosomal translocation;
CC Polymorphism; Disease mutation.
KW

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FT DOMAIN 10 30 BH4.
FT 93 107 BH3.
FT 136 155 BH1.
FT 187 202 BH2.
FT 212 233 POTENTIAL.
FT 34 35 CLEAVAGE (BY CASPASE-3).
FT MOD_RES 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
FT VASAPLIC 196 239 DAFVEELGSPMRPLEDSWTLSTLSTLAVGACITLAVL
FT VARIANT 7 7 T -> S.
FT VARIANT 7 7 /FTID=VAR_000827.
FT VARIANT 59 59 P -> S (IN NON-HODGKINS-LYMPHOMA; SOMATIC
FT VARIANT 59 59 /FTID=VAR_000828.
FT VARIANT 93 93 V -> I (IN NON-HODGKINS-LYMPHOMA; SOMATIC
FT MUTAGEN 34 34 /FTID=VAR_000829.
FT MUTAGEN 64 64 D->A: ABOLISHES CLEAVAGE BY CASPASE-3.
FT MUTAGEN 145 145 G->A: NO EFFECT ON CLEAVAGE BY CASPASE-3.
FT MUTAGEN 145 145 G->A: NO HETERODIMERIZATION WITH BAX AND
FT MUTAGEN 188 188 LOSS OF ANTI-APOPTOTIC ACTIVITY.
FT MUTAGEN 188 188 W->A: NO HETERODIMERIZATION WITH BAX AND
FT CONFLICT 48 48 LOSS OF ANTI-APOPTOTIC ACTIVITY.
FT CONFLICT 59 59 I -> F (IN REF. 4).
FT CONFLICT 117 117 P -> T (IN REF. 3).
FT CONFLICT 129 129 S -> R (IN REF. 3).
FT SEQUENCE 239 AA; 26266 MW; 3C49F2B71ADC9C6B CRC64;
SO

```

Query Match 7.8%; Score 116; DB 1; Length 239;  
Best Local Similarity 19.4%; Pred. No. 0.0027;  
Matches 48; Conservative 39; Mismatches 76; Indels 84; Gaps 10;

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QY 79 DIEFVVDYFTHRRONGMCF----- 100
DB 10 DNREIVKYLHYKLSQGYEMDAGVGAPGAPGIFSSOPGTHPHPASRDVART 69
QY 101 -----GAPGLPCG-----VQP-EHEMRYMGTFIEFKHNEPTCEOLAVPRISFL 148
DB 70 SPLQTPAPAPAAAGPALSPPYPVHLTLKRAQGDSESRIRRDRAEMSSQHLTPFAROR 129
QY 149 YQDYVFTVGNAGTDCPMSTYGRILGLISFGFYAARMMSV--ELQGVNLEFVYTSLEPT 206
DB 130 FAFYVE-----ELFRDGVNMGRIVAFFEEFGVNC--VESVNEMSPVDNALMWTETVL 181
QY 207 KTRLRNNKKEHNSWDDEMTL-GKOMKEDYERAEAKVGRNRNRW-----SMIG 256
DB 182 NRHL-HTWIDNGMDAFVELYGPMSRPLEDS-----WLSLKTLLSLALVG 227
QY 257 AGVTAGA 263
DB 228 ACITLGA 234

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RESULT 14

ID	BCL2_RAT	STANDARD;	PRT;	236 AA.
AC	P49950; O62837; O64032;			
DT	01-OCT-1996 (Rel. 34. Created)			
DT	01-NOV-1997 (Rel. 35. Last sequence update)			
DT	15-JUN-2002 (Rel. 41. Last annotation update)			
DE	Apoptosis regulator Bcl-2.			
GN	BCL2 OR BCL-2.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_Taxid=10116;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=94193015; PubMed=8144041;			
RA	Sato T., Irie S., Krajewski S., Reed J.C.; the rat Bcl-2 protein."			
RT	"Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein."			

RL Gene 140:291-292(1994).  
 RP [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Ovary;  
 RX MEDLINE=95129487; PubMed=7828536;  
 RA Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;  
 RT "Expression of members of the bcl-2 gene family in the immature rat  
 RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa  
 RT cell apoptosis is associated with decreased bax and constitutive  
 RT bcl-2 and bcl-x long messenger ribonucleic acid levels.";  
 RL Endocrinology 136:232-241(1995).  
 RN [3]  
 RP SEQUENCE OF 19-172 FROM N.A.  
 RX MEDLINE=95059917; PubMed=7969891;  
 RA Castren E., Ohga Y., Berzaghi M.P., Tzimagiorgis G., Thoenen H.,  
 RA Lindholm D.;  
 RT "bcl-2 messenger RNA is localized in neurons of the developing and  
 RT adult rat brain.";  
 RL Neuroscience 61:165-177(1994).  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 CC including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (APAF-1).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2  
 CC domains, and is necessary for anti-apoptotic activity (By  
 CC similarity). Also interacts with APAF-1 and RAIF-1 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 CC membrane of the nuclear envelope and the endoplasmic reticulum.  
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues, with  
 CC highest levels in reproductive tissues. In the adult brain,  
 CC expression is localized in mitral cells of the olfactory bulb,  
 CC granule and pyramidal neurons of hippocampus, pontine nuclei,  
 CC cerebellar granule neurons, and in ependymal cells. In prenatal  
 CC brain, expression is higher and localized in the neuroepithelium  
 CC and in the cortical plate.  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
 CC for interaction with RAIF-1 (By similarity).  
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and  
 CC occurs during the G2/M phase of the cell cycle. In the absence of  
 CC growth factors, Bcl2 appears to be phosphorylated by other protein  
 CC kinases such as ERKs and stress-activated kinases.  
 CC -1- PTM: Phosphorylated by protein phosphatase 2A (PP2A) (By similarity).  
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 CC activity, causes the release of cytochrome c into the cytosol  
 CC promoting further caspase activity (By similarity).  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: L14680; AAA53662.1; -;  
 CC EMBL: U34964; AAA77687.1; -;  
 CC EMBL: S74122; -; NOT\_ANNOTATED\_CDS.  
 CC HSSP: 007817; 1MAZ.  
 CC InterPro: IPR002475; BCL2\_family.  
 CC InterPro: IPR000712; BCL2\_BH.  
 CC InterPro: IPR003093; BCL2\_BH4.

DR InterPro: IPR004725; Bcl2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRFAMs: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4; 1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 DR Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.  
 FT DOMAIN 10 30  
 FT DOMAIN 90 104 BH3.  
 FT DOMAIN 133 152 BH1.  
 FT DOMAIN 184 199 BH2.  
 FT TRANSMEM 209 230  
 FT SITE 34 35  
 FT MOD\_RES 70 70  
 FT CONFLICT 42 42 A -> R (IN REF. 2).  
 FT CONFLICT 157 157 S -> G (IN REF. 1).  
 FT CONFLICT 164 164 S -> Y (IN REF. 2).  
 FT CONFLICT 212 212 L -> Q (IN REF. 2).  
 SQ SEQUENCE 236 AA; 26622 MW; E7688CB9071A872A CRC64;  
 Query Match 7.7%; Score 114.5; DB 1; Length 236;  
 Best Local Similarity 19.2%; Pred. No. 0.0036; Mismatches 75; Indels 83; Gaps 10;  
 Matches 47; Conservative 40;  
 QY 79 DIGEVDVYDTHIRONGMEM-----FGAGLPCGYOP----- 112  
 DB 10 DNEIYWKYIHVLSRGYEMDGDSDASAPLRAPRPGI-FSQPSNNTPAVHRPTAAR 68  
 QY 113 -----HEMMRWGTFTEKKHAENFETFCQLAVPRISLYQ 150  
 DB 69 TSPRLPVLAVNAGPALSPVPVHLTLFRAGDDFSRRYRDFEMSSQLHTEFTANGRA 128  
 QY 151 DVRTVGNAGTDDCPMSYGRLLGLISFGGTVAKKMEV--ELGGVRNLFVYTSLFIT 208  
 DB 129 TVVE-----ELFRDGVNMGRIVAFFERGGVVC--VESVNRRESPLVDNALMTEYLNR 180  
 QY 209 RIRNNMKEHNRSDDEPTLT-GKQKEDYERAEAKVGRKRNRR-----SMIGAG 258  
 DB 181 HL-HTWQDNGMDAFVELXGPMRLPDRS-----WLSKTLTSLALVGC 226  
 QY 259 VTAGA 263  
 DB 227 ITLGA 231  
 RESULT 15  
 BCLX\_CHICK STANDARD; PRT; 229 AA.  
 ID BCLX\_CHICK  
 AC Q07816; Q98908;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-X.  
 GN BCL2L1 OR BCLX OR BCL-X.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A. (SHORT FORM).  
 RX MEDLINE=93364977; PubMed=8358789;  
 RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,  
 RA Turka L.A., Mao X., Nunez G., Thompson C.B.;  
 RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator  
 RT of apoptotic cell death.";  
 RL Cell 74:597-608(1993).



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OM protein - protein search, using sw model

Run on: February 24, 2003, 11:51:59 : Search time 33 seconds

(without alignments)  
1748.279 Million cell updates/sec

Title: US-09-993-420A-3  
Perfect score: 1479  
Sequence: 1 MRCGTADNLTNPAYRRRTM.....AGATGCVGVCGRMFSLK 280

Scoring table: BLOSOM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp.\_archaea:\*  
2: sp.\_bacteria:\*  
3: sp.\_fungi:\*  
4: sp.\_human:\*  
5: sp.\_invertebrate:\*  
6: sp.\_mammal:\*  
7: sp.\_mhc:\*  
8: sp.\_organelle:\*  
9: sp.\_phage:\*  
10: sp.\_plant:\*  
11: sp.\_rodent:\*  
12: sp.\_virus:\*  
13: sp.\_vertebrate:\*  
14: sp.\_unclassified:\*  
15: sp.\_vivirus:\*  
16: sp.\_bacteriophage:\*  
17: sp.\_archaeop:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	151	10.2	193	11	088996
2	139	9.4	233	6	088996
3	136	9.2	233	6	088996
4	134	9.1	233	6	09MTW4
5	132	8.9	233	6	09N1A2
6	130	8.8	233	6	09M2S7
7	124.5	8.4	178	11	035844
8	124.5	8.4	217	11	09CWM5
9	124	8.4	180	6	09BD5
10	124	8.4	180	6	09BD5
11	117.5	7.9	238	13	090298
12	110.5	7.5	236	11	0923R6
13	108	7.3	1329	16	088996
14	99	6.7	177	13	0902N1
15	99	6.7	188	4	09H1R6
16	99	6.7	331	11	P97287

17	98	6.6	330	11	0921P3
18	96.5	6.5	757	16	0914S8
19	96	6.5	188	11	090WX2
20	96	6.5	235	11	035843
21	95	6.4	350	4	090ND1
22	93	6.3	176	13	08UWD5
23	91.5	6.2	463	5	09N960
24	91.5	6.2	639	10	09FLA9
25	90.5	6.1	279	16	08X369
26	90.5	6.1	644	16	08UC9
27	89.5	6.1	211	13	09W6F1
28	89	6.0	101	11	09CR14
29	88.5	6.0	219	11	099N36
30	88.5	6.0	283	16	08X3U5
31	88	5.9	255	13	0919N3
32	87.5	5.9	104	11	09R289
33	87.5	5.9	152	6	09SKR3
34	86	5.8	326	17	08TIP1
35	86	5.8	384	16	09CFX9
36	85.5	5.8	961	16	08R608
37	85	5.7	1353	4	09Y4B5
38	85	5.7	2368	2	093T96
39	85	5.7	2904	11	09EPN0
40	85	5.7	2931	11	09EPN9
41	85	5.7	2936	11	09EPN1
42	84.5	5.7	150	16	09PP87
43	84.5	5.7	430	16	09HXP6
44	84.5	5.7	559	5	09NG26
45	84.5	5.7	568	5	09VEB6

## ALIGNMENTS

RESULT 1					
ID	088996	PRELIMINARY:	PRT:	193 AA.	
AC	088996:				
DT	01-NOV-1998 (TREMBLrel. 08, Created)				
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE	Bcl-w.				
GN	BCL-W.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;				
RX	MEDLINE=99292146; PubMed=10366024;				
RA	Hammer S., Skoglova Y., Lindholm D.;				
RT	"Differential expression of bcl-w and bcl-x messenger RNA in the				
RT	developing and adult rat nervous system.";				
RL	Neuroscience 91:673-684(1999).				
DR	EMBL: AF096291; AAC64200.1; -.				
DR	HSSP: 007817; IMZ.				
DR	InterPro: IPR000712; BCL2_BH.				
DR	InterPro: IPR003093; BCL2_BH4.				
DR	InterPro: IPR002475; BCL2_Family.				
DR	Pfam: PF00452; Bcl-2; 1.				
DR	Pfam: PF02180; BCL; 1.				
DR	SMART: SM00337; BCL; 1.				
DR	SMART: SM00265; BH4; 1.				
DR	SMART: PS50062; BCL2_FAMILY; 1.				
DR	PROSITE: PS01080; BH1; 1.				
DR	PROSITE: PS01258; BH2; 1.				
DR	PROSITE: PS01260; BH4; 1.				
DR	PROSITE: PS50063; BH4_2; 1.				
DR	SEQUENCE 193 AA; 20820 MW; 36D6742F4529AFB4 CRC64;				
Query Match	10.2%;	Score 151;	DB 11;	Length 193;	
Best Local Similarity	24.3%;	Pred. No. 1.8e-06;			



RESULT 5			
Q9M2S7			
ID	Q9M2S7	PRELIMINARY:	PRT: 233 AA.
AC	Q9M2S7;		
DT	01-OCT-2000 (TREMBLrel. 15, Created)		
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	Bcl-x long protein.		
OS	Ovis aries (Sheep).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae		
OC	Bovidae; Caprinae; Ovis.		
OX	NCBI_TaxID=9940;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=OVARY;		
RA	Murray J.F., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.;		
RT	"Bcl-x in the sheep ovary";		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF164517; AAF99533.1; -.		
DR	HSSP: P53563; IAF3.		
DR	InterPro: IPR000712; Bcl2_BH.		
DR	InterPro: IPR003093; Bcl2_BH4.		
DR	InterPro: IPR002475; Bcl2_family.		
DR	InterPro: IPR004725; Bcl2_leg.		
DR	Pfam: PF00452; Bcl-2_1.		
DR	Pfam: PF02180; BH4_1.		
DR	SMART: SM00337; BCL; 1.		
DR	SMART: SM00265; BH4; 1.		
DR	TIGRfams: TIGR00865; bcl-2_1		

ID	035844	PRELIMINARY:	PRT:	233 AA.
AC	035844;			
DT	01-JAN-1998 (TrEMBLrel. 05, Created)			
DT	01-JAN-1998 (TrEMBLrel. 05, Last sequence update)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DE	Bcl-2L.			
GN	Bcl2L.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=B6/CBA; TISSUE=THYMUS;			
RC	MEDLINE=98051053; PubMed=9390687;			
RA	Yang X.-F., Weber G.F., Cantor H.;			
RT	"A novel Bcl-x isoform connected to the T cell receptor regulates			
RT	apoptosis in T cells."			
RL	Immunity 7:629-639(1997).			
DR	EMBL; U51278; AAC53459.1; -.			
DR	HSSP: P53563; IAP3.			
DR	MCD; MGI:88139; Bcl2L.			
DR	InterPro: IPR000712; Bcl2_BH.			
DR	InterPro: IPR003093; Bcl2_BH4.			
DR	InterPro: IPR002475; Bcl2_BH4.			
DR	InterPro: IPR004725; Bcl2_reg.			
DR	Pfam: PF00452; Bcl-2; 1.			
DR	Pfam: PF02180; BH4; 1.			
DR	SMART; SM00337; BCL; 1.			
DR	SMART; SM00265; BH4; 1.			
DR	TIGRFAMs; TIGR00865; bcl-2; 1.			
DR	PROSITE; PS50062; BCL2_FAMILY; 1.			
DR	PROSITE; PS01080; BH1; 1.			
DR	PROSITE; PS01258; BH2; 1.			
DR	PROSITE; PS01259; BH3; 1.			
DR	PROSITE; PS01260; BH4; 1; 1.			
DR	PROSITE; PS00663; BH4_2; 1.			
SO	SEQUENCE 233 AA; 26033 MW; 3083F2D8327E072E CRC64;			

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Query Match      8.8%; Score 130; DB 11; Length 233;
Best Local Similarity 20.9%; Pred. No. 0.00024;
Matches 52; Conservative 38; Mismatches 83; Indels 76; Gaps 10;

OY 84 VVDYFTHRRIRONGMMEF-----GA 102
   ||:||||:|
DB 9 VVDFLSYKLSQKYSWSQSDVEENRTEAPEETEARERPSAINGNPSWHLADSPAVNCA 68
   ||:||||:|
OY 103 PGLPCVQPEH-----EMRMVGTIEFEKHAENFETCEOLLAVPRISFLYDQVVR 154
   ||:||||:|
DB 69 TGHSSSLDAREVTPMAVVAQALREAGDEFELRYRRAFSDLTSQLHTPTGAYOSFEQVYN 128
   ||:||||:|
OY 155 TVGNAQTDCPMYSYRLLIGLISFGFVAAKMPV--ELQGVYRNLFVYTSLFKTRIRN 212
   ||:||||:|
DB 129 -----ELFRDGVNMGRIIVAFSEFG--ALCVESVDKEMQVLVSRIASMMATYLNHDL-E 179
   ||:||||:|
OY 213 NKEHHRSMDEFTLGKQKMEDEY-ERAEAEKVRKRRKONRSMIGAVTGAIQVGVVY 271
   ||:||||:|
DB 180 PVIQENGGMOTFVDL-----YGNNAAESRKRGEGFNWFLTG-----MTVAGVVL 225
   ||:||||:|
OY 272 CGRMFSLK 280
   ||:||||:|
DB 226 LG-SLFSRK 233

RESULT 7
O9CYW5 PRELIMINARY; PRT; 178 AA.
AC O9CYW5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Bcl2-1-like 2.
GN BCL2L2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido T., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J.,ombaerts P.,
RA Nordone P., Ring B., Ringuwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
EMBL: AK013244; BAB28740.1; -.
DB HSSP: 007817; IMAZ.
MCD: MGI:108052; Bcl2L2.
InterPro: IPR000712; Bcl2_BH.
InterPro: IPR003093; Bcl2_BH4.
InterPro: IPR002475; BCL2_family.
Pfam: PF00452; Bcl-2; 1.
Pfam: PF02180; BH4; 1.
SMART: SM00337; BCL; 1.
SMART: SM00265; BH4; 1.

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DR PROSITE: PSS0062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PS0063; BH4_2; 1.
SQ SEQUENCE 178 AA; 19147 MW; E2D4C3F79528E9D7 CRC64;

Query Match      8.4%; Score 124.5; DB 11; Length 178;
Best Local Similarity 24.8%; Pred. No. 0.00056;
Matches 38; Conservative 23; Mismatches 65; Indels 27; Gaps 5;

OY 79 DIEGFVDFYTHRRIRONGMMEFAGPLPCGVQPEHEHMRVMTIEFEKHAENFETCEOL 138
   ||:||||:|
DB 9 DTRALVADFEVGYKRLQKGYVCAGPGEPADPLHQIMRAAGDEFETRRFTSDLAOL 68
   ||:||||:|
OY 139 LAVP-----RISFLYDVRVRYGNMOTDQCPMSYGRLLIGLISGFVAAKMP--ES 188
   ||:||||:|
DB 69 HVTGSAOQRFQVSDLEFQ-----GPNWGRVAFVFGALCAESVAKEM 115
   ||:||||:|
OY 189 VELQGVYRNLFVYTSLFKTRIRNNKEHNRV 221
   ||:||||:|
DB 116 EPLVGVQDMV--AYLETRLA-DWTHSSGW 144

RESULT 8
O99N35 PRELIMINARY; PRT; 217 AA.
AC O99N35;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE B-cell leukemia/Lymphoma x (Fragment).
GN BCLX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Yang X.-F., Cantor H.;
RT "Novel cDNA structure and genomic organization of apoptosis regulatory
RT gene Bcl-x-gamma.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DB EMBL: AF133282; AAK15455.1; JOINED.
DB EMBL: AF133281; AAK15455.1; JOINED.
DR HSSP: P35363; IAF3.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR TIGRFAMs: TIGR00865; bcl-2; 1.
DR PROSITE: PSS0062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
FT NON_TER 1
SQ SEQUENCE 217 AA; 24234 MW; 3B5A4E809A7DEF18 CRC64;

Query Match      8.4%; Score 124.5; DB 11; Length 217;
Best Local Similarity 25.3%; Pred. No. 0.00074;
Matches 43; Conservative 33; Mismatches 67; Indels 27; Gaps 8;

OY 114 EMRMVGTIEFEKHAENFETCEOLLAVPRISFLYDQVRYTGNMOTDQCPMSYGRLLIG 173
   ||:||||:|
DB 72 QALREAGDEFELRYRRAFSDLTSQLHTPTGAYOSFEQVYN-----ELFRDGVNMGRIVA 126
   ||:||||:|
OY 174 LISFGFVAAKMPV--ELQGVYRNLFVYTSLFKTRIRNNKEHNSWPDFTLGKQ 231
   ||:||||:|
DB 127 FFSEFG--ALCVESVDKEMQVLVSRIASMMATYLNHDL-EPVLIQENGGMOTFVDL----- 178
   ||:||||:|
OY 232 KEDY-ERAEAEKVRKRRKONRSMIGAVTGAIQVGVVCGRMFSLK 280
   ||:||||:|

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Db 179 ---YGNNAAESRKGOERFNRWFLTG-----MTVAGVLLG-SLFSRK 217

## RESULT 9

Q9BDD5 PRELIMINARY; PRT; 180 AA.  
 AC Q9BDD5; 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)  
 DE Anti-apoptotic regulator Bcl-XL (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
 OC Bovidae; Bovinae; Bos.  
 NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Amills M., Bouzat J.;  
 RT "Characterization of the bovine bcl-xl gene and related pseudogenes."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF245488; AAK31307.1; -  
 DR EMBL: AF245489; AAK31308.1; -  
 DR HSSP: Q07817; IMAZ.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PS00062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 FT NON\_TER 1 180  
 FT NON\_TER 1 180  
 SQ SEQUENCE 180 AA; 20062 MW; 95DC436F95DABDA6 CRC64;  
 Query Match 8.4%; Score 124; DB 6; Length 180;  
 Best Local Similarity 24.2%; Pred. No. 0.00064;  
 Matches 40; Conservative 33; Mismatches 66; Indels 26; Gaps 7;  
 QY 114 EMNRWAGTTEKKHAENFEFCQQLAVPRISFLYQDVYRTYGNACTQCPMSYRRLIG 173  
 Db 38 QALREAGDEFEELRYRRAFSDLTSQHLITPGTAYQSEOVVN-----ELFRDGVNNGRIYA 92  
 QY 174 LISFGFVAAKKMESV--ELQGVNRLFVYTSLEFTRIRNNKKEHNRSWDDPMTLGKM 231  
 Db 93 FFEFGG---ALCVESYDKEMQVLSRIATWATYINDHL-EPYIQNGGMDTFVEL----- 144  
 QY 232 KEDY-ERAERAEKVRKKNRSMIGAGVTAGIIVGVVCGRM 275  
 Db 145 ---YGNNAAESRKGOERFNRWFLTG-----MTVAGVLLGSL 179  
 RESULT 10  
 Q9BDD5 PRELIMINARY; PRT; 180 AA.  
 AC Q9BDD5; 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)  
 DE Anti-apoptotic regulator Bcl-XL (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
 OC Bovidae; Bovinae; Bos.  
 NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Amills M., Bouzat J.;  
 RT "Characterization of the bovine bcl-xl gene and related pseudogenes."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF245487; AAK31306.1; -  
 DR HSSP: Q07817; IMAZ.

DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PS00062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 FT NON\_TER 1 180  
 FT NON\_TER 1 180  
 SQ SEQUENCE 180 AA; 20056 MW; 62C4C0BD055A9EF CRC64;

Query Match 8.4%; Score 124; DB 6; Length 180;  
 Best Local Similarity 23.9%; Pred. No. 0.00064;  
 Matches 45; Conservative 35; Mismatches 70; Indels 38; Gaps 9;

QY 101 GARG-----LPCGVQPEHEMRWAGTTEKKHAENFEFCQQLAVPRISFLYQ 150  
 Db 17 GAPGSRSSDAREVIP--MAAVKQALREAGDEFEELRYRRAFSDLTSQHLITPGTAYQSE 74  
 QY 151 DVVFRVGNACTQCPMSYGRLLISFGGFVAAKKMESV--ELQGVNRLFVYTSLEFTRIR 208  
 Db 75 QVYN-----ELFRDGVNNGRIYASFSG---ALCVESYDKEMQVLSRIATWATYIND 126  
 QY 209 RIRNNWKEHNRSWDDPMTLGKQMKEDY-ERAERAEKVRKKNRSMIGAGVTAGIIV 267  
 Db 127 HL-EPWIDENGMDTFVEL-----YGNNAAESRKGOERFNRWFLTG-----MTVA 171  
 QY 268 GVVVCGRM 275  
 Db 172 GVLLGSL 179

## RESULT 11

Q90298 PRELIMINARY; PRT; 238 AA.  
 AC Q90298; 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)  
 DE Bcl-XL-like protein 1.  
 GN Bclp.  
 OS Brachydanio rerio (zebrafish) (zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21299061; PubMed=11406282;  
 RA Chen M.-C., Gong H.-Y., Cheng C., Wang J.-P., Hong J., Wu J.-L.;  
 RT "Cloning and characterization of zfbp1, a Bcl-XL homologue from the zebrafish, Danio rerio(1)."  
 RL Blochim. Biophys. Acta 1519:127-133(2001).  
 DR EMBL: AF317837; AAK81706.1; -  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR003093; BCL2\_BH4.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR PROSITE: PS00062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; UNKNOWN\_1.  
 DR PROSITE: PS00063; BH4\_2; 1.  
 SQ SEQUENCE 238 AA; 26253 MW; 658394933EEFDB CRC64;  
 Query Match 7.9%; Score 117.5; DB 13; Length 238;  
 Best Local Similarity 23.4%; Pred. No. 0.0039;  
 Matches 39; Conservative 38; Mismatches 69; Indels 21; Gaps 7;  
 QY 108 GYQPEHEMRWAGTTEKKHAENFEFCQQLAVPRISFLYQDVYRTYGNACTQCPMS 167  
 Db 85 GIDAVKALRDSANFEELRYRRAFSDLTSQHLITPATYQSEFSDV-----FRGVN 139  
 QY 168 YGRLIGLISFGGFVAAKKMESV--ELQGVNRLFVYTSLEFTRIRNNKKEHNRSWDDPMTL 227

Db 140 WGRIVOLFAGALVCEVEK-EMSPVLRVIAEMTVYLDNHQ-PWISQSGWEPFAL 197  
 QY 228 -GKQKEDYERAEKVGRRKORRSMIGAGTGAIGVGVCG 273  
 Db 198 FGKD-----AAESRKSQESRKKM-LFAGMTL-----LTGVVGG 231

## RESULT 12

Q923R6 PRELIMINARY: PRT: 236 AA.

AC Q923R6;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE B-cell lymphoma protein 2.  
 GN BCL2.  
 OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Cricetulus.  
 OC NCBI\_Taxid=10030;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lai D.Z., Chen W., Wang H.T.;  
 RT "Construction of a robust CHO cell line for biopharmaceutical use."  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF040339; AAK92201.1;  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH4.  
 DR InterPro: IPR002475; Bcl2\_family.  
 DR InterPro: IPR004725; Bcl2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR TIGRfams: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; UNKNOWN\_1.  
 DR PROSITE: PS01258; BH2; UNKNOWN\_1.  
 DR PROSITE: PS01259; BH3; UNKNOWN\_1.  
 DR PROSITE: PS01260; BH4\_1; UNKNOWN\_1.  
 DR PROSITE: PS50063; BH4\_1; UNKNOWN\_1.  
 DR PROSITE: PS50063; BH4\_1; UNKNOWN\_1.  
 SQ SEQUENCE 236 AA; 26500 MW; BEDF052EF32CA8B8 CRC64;

Query Match 7.5%; Score 110.5; DB 11; Length 236;  
 Best Local Similarity 19.3%; Pred. No. 0.018;  
 Matches 47; Conservative 41; Mismatches 73; Indels 83; Gaps 11;

QY 79 DIEGFVVDYFTHRIKQNGEM-----FGA---PGLPGVQPE----- 112  
 Db 10 DNREIVMKYIHYKLSORGYEMDVGDDVDAPLGAAPTGI-FSQPESNPPPAVHRDMAR 68  
 QY 113 -----HEMRYMGTIFEKKAENFEFCQOLLAVRISFSLYQ 150  
 Db 69 TSPLRPIVATTGPTLSPVPVYVHLTKRAGDDFSRRYRDRDAEMSSQHLPTARGRFA 128  
 QY 151 DVRTVGNAGTDQCPMSYGRLLIGLISFGFVAAKMESV--ELQGVNLFVYTSLYKT 208  
 Db 129 TVVE-----ELFRDGVNNGRIYAFEEFQVVC---VESVNRMSPLVIALMTETYLNR 180  
 QY 209 RIRNNKKEHNSWDDFMTL-GKQKEDYERAEKVGRRKORR-----SMIGAG 258  
 Db 181 HL-HTWIODNGMDAFVELYGPSVAPLPDFS-----WLSLTLLNLALVAGAC 226  
 QY 259 VTAG 262  
 Db 227 ITLG 230

RESULT 13  
 Q8YTT7 PRELIMINARY: PRT: 1329 AA.  
 AC Q8YTT7;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE WD-repeat containing protein.  
 GN AL0759.  
 OS Anabaena sp. (strain PCC 7120).  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
 OC NCBI\_Taxid=103690;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21595285; PubMed=11759840;  
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,  
 RA Watanabe A., Iriuguchi M., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
 RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,  
 RA Yasuda M., Tabata S.;  
 RT "Complete genomic sequence of the filamentous nitrogen-fixing  
 cyanobacterium Anabaena sp. strain PCC 7120."  
 RL DNA Res. 8:205-213(2001).  
 DR EMBL: AF003583; BAB72716.1;  
 DR InterPro: IPR001680; WD40.  
 DR Pfam: PF00400; WD40; 15.  
 DR PRINTS: PR00320; GPROTEINBRPT.  
 DR SMART: SM00320; WD40; 16.  
 DR PROSITE: PS00678; WD\_REPEATS\_1; UNKNOWN\_7.  
 DR PROSITE: PS50082; WD\_REPEATS\_2; 5.  
 DR PROSITE: PS50294; WD\_REPEATS\_REGION; 1.  
 DR Complete proteome.  
 SQ SEQUENCE 1329 AA; 148584 MW; 0AE2DC35BEED07359 CRC64;

Query Match 7.3%; Score 108; DB 16; Length 1329;  
 Best Local Similarity 22.7%; Pred. No. 0.33;  
 Matches 68; Conservative 39; Mismatches 101; Indels 92; Gaps 14;

QY 12 NPAYRRRTATGEMKEFLGKTEPTFGINSDAQDLPSPRQASTRR-MSIGESI--DG 68  
 Db 173 NPAYRRRTATGEMKEFLGKTEPTFGINSDAQDLPSPRQASTRR-MSIGESI--DG 68  
 QY 69 -KINDWEPRLDIEGFVVDYFTHRIKQNGEMFGAPGPCVQ----- 110  
 Db 212 FKIDHIEPLAKGLAGKEN--PQAVMOEVLAVTG--GQPLITQVCELGKALSIERKF 267  
 QY 111 ---PEHEMRYMGTIFEKKAENFE-----TFCEQLLAVPRIS---FSLYQDVYRT 155  
 Db 268 RSVDENGIIELVKELIHNQIIDNWEANDKQEHKTRIRLLISEISVALLGQQLIQ 327  
 QY 156 VGNAGTDQCPMSYGRLLIGLISFGFVAAKMESVLEQGVNLFVYTSLYKTIRIRN- 213  
 Db 328 VEMTADSSFEQMRRLTGLV-----VQOQKLRVYNOIYRNVPDLSEWENEL 374  
 QY 214 -----WKEHNSWDDFMTLGRKQKEDYERAEKVGRRKORRSMIGAGVTA 261  
 Db 375 GKLRFYADKLRAWESNIDQNTCLMG-----EDLEKARVADGKRLSDVDRFLSASVEA 430

## RESULT 14

Q90ZNI PRELIMINARY: PRT: 177 AA.

AC Q90ZNI;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Anti-apoptotic NR13.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_Taxid=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Gillet G., Lalle P., Miscopein A.;  
 RT "Electrostatic interactions between Bcl-2 homology domains BH3 and BH4  
 are essential for NR13 anti-apoptotic activity."  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

115 -----MMRVGMTIEKHAENFETCEQLLAVPRIISLYQDVVR 154

Search completed: February 24, 2003, 11:54:41  
Job time : 36 secs

